Sequence:

Run on:

Sequence 1, Appli Sequence 1, Appli Sequence 551, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 11285, A Sequence 11285, A Sequence 11302, A

Sequence 3, Appli Sequence 3, Appli Sequence 5, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli

Sequence 1, Appli Sequence 1899, Ap Sequence 1168, Ap

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3 IlePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaAsp-SerSe 22 ::: ::: ::: |||||||:::
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Sequence 66, Application US/09370838

Patent No. 6444425

GENERAL INFORMATION:
APPLICANT: Red, Steven G.
APPLICANT: Mohamath, Roadoh
ITILE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE FILE REFERENCE: 210121.47521
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT PILING DATE: 1999-08-09
RARLIER APPLICATION NUMBER: US 09/285,323
FRALIER FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
NUMBER OF SEQ ID NOS: 289
SOFTWARE: FastSEQ for Windows Version 3.0
                       US-08-750-163-1

US-08-256-799-1

US-08-256-799-1

US-08-256-799-1

US-09-462-437-1

US-09-489-039A-5551

US-09-489-039A-5551

US-09-621-976-13459

US-09-626-047-5

US-09-626-047-5

US-09-626-047-5

US-09-626-047-5

US-09-626-047-5

US-09-626-047-5

US-09-620-0120-01

US-09-52-991A-11285

US-09-52-991A-11285

US-09-52-188-19

US-09-52-188-19

US-09-625-188-19

US-09-645-178-12

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Mismatches:
Indels:
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Matches:
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35.09%
21.99%
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US-09-370-838-66
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Best Local Similarity:
Query Match:
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-MODEL=frame+ par.model.-DEV=xlh
-Q=/cgn2_1/USPTO_spool/USI0079754/runat_06082004_181229_29419/app_query.fasta_1.199
-Q=/cgn2_1/USPTO_spool/USI0079754/runat_06082004_I81229_29419/app_query.fasta_1.199
-Q=/cgn2_1/USPTO_spool/USI0079754-runat_0-MINNATCH=0.1 -LOOPGL=0.
-LOOPEXT=0.-UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -TRR SCORE=pot -TRR MAX=100 -TRR MINN-0 -ALIGN=15
-MODEL-CAL.-OUTFMT=pot -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=USI0079754 GOCGN 1 1 6 9 crunat_06082004_181229_29419 -NOPU=6 -ICPU=3
-NO MWAP -LARGEQUERY -NEG_SCORES= 0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=90 -TRREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DSLEXT=7
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Sequence 2, Appli
Sequence 1, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 17, Appl
Sequence 17, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 31, Appli
Sequence 30, Appli
Sequence 30, Appli
                                                                                                                                                                                                             August 15, 2004, 22:31:28 ; Search time 60 Seconds (without alignments) 536.453 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                         1 MKIFIFVFIMALILAMIRAD......0QYQPYQRYPLNYPPAYPFP 58
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11. \cgn2_6/ptodated_2/ina/5A_COMB.seq:*
12. \cgn2_6/ptodated_2/ina/5B_CCMB.seq:*
13. \cgn2_6/ptodated_2/ina/6A_COMB.seq:*
14. \cgn2_6/ptodated_2/ina/6B_COMB.seq:*
15. \cgn2_6/ptodated_2/ina/PCTUS_COMB.seq:*
15. \cgn2_6/ptodated_2/ina/PCTUS_COMB.seq:*
16. \cgn2_6/ptodated_2/ina/PCTUS_COMB.seq:*
16. \cgn2_6/ptodated_2/ina/PcTUS_COMB.seq:*
17. \cgn2_6/ptodated_2/ina/PcTUS_COMB.seq:*
18. \cgn2_6/ptodated_2/ina/PcTUS_COMB.seq:*
18. \cgn2_6/ptodated_2/ina/Packfiles1.seq:*
                                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                          OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2581 4 US-09-370-838-66

3164 4 US-09-023-655-816

9 4415755 3 US-09-103-840A-2

6 2335 3 US-09-103-840A-1

6 2335 4 US-09-387-574-9

6 2335 4 US-09-68-096-9

3 4379 1 US-08-522-214A-17

1 4413765 3 US-09-103-840A-1

1 4411529 3 US-09-103-840A-1

1 4411529 3 US-09-103-840A-1

9 750 4 US-09-359-301A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               682709 seqs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Database :

21100076543

Result No.

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1189176 CGTTGCCATACAGCAGCCCACCGCCGCCGCCGCCGCCGCCGCCGCCGA 1189235
                                         22 rGluGlu-LysArgHisArgLysArgLysHis---HisArgGlyTyrPheGlnGlnT 41
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Fatent No. 629423

GENERAL INFORMATION:

APPLICANT: FLEISCHMAN, Robert D.

APPLICANT: WHITE, Owen R.

APPLICANT: FRASER, Claire M.

APPLICANT: FRASER, Claire M.

APPLICANT: WENTER, John C.

TITLE OF INVENTION: TUBERCULOSIS

FILE REFERENCE: 24366-20007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT APPLICATION NUMBER: US/09/103,840A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 ArgAlaAspSerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyr 37
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FLEISCHAM, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 2456-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
                                                                                                                                               1104 CTCGTCCTCGTCATCCTCATCTTCATCATCTCTCGGACTCCG 1058
                                                                                                           41 yrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyrPro 56
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Matches:
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ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/09103840A; Patent No. 6294328; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTHER INFORMATION: CDC 1551
CTHER INFORMATION: "n" bases at
CTHER INFORMATION: represent a,
US-09-103-840A-2
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32.26%
20.89%
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LENGTH: 4411529
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38 ----
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                   18 ArgAlaAspSerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyr 37
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Sequence 9, Application US/09387574

Sequence 9, Application US/09387574

GENERAL INFORMATION:
APPLICANT: Kinney, Tony
APPLICANT: Kinney, Tony
ITILE OF INVENTION: Plant Geranylgeranyl Transferases
FILE REFERENCE: BB-1239

FILE REFERENCE: BB-1239

CURRENT APPLICATION NUMBER: US/09/387,574

CURRENT FILING DATE: 1999-08-31

EARLIER APPLICATION NUMBER: 60/098,743

EARLIER PILING DATE: September 1, 1998

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Microsoft Office 97

FEARLIER PLANTAL OFFICE OFFICE
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Matches:
Conservative:
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Indels:
                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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34.15%
25.61%
20.57%
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ORGANISM: Oryza sativa
US-09-387-574-9
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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                                               Alignment Scores:
Pred. No.:
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US-09-103-840A-1
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US-09-387-574-9
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Patent NO. 5811536
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identify
TITLE OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES:
ADDRESSES: AADDRESS:
AADDRESSES: CAMBEDELI and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                         JOHNERAL INFORMATION, Rebecca E.
APPLICANT: Kinney, Tony
APPLICANT: Kinney, Tony
APPLICANT: Rafalski, Antoni
APPLICANTON: Plant Geranylgeranyl Transferases
FILE REFRENCE: BB1239 US NA DIV
CURRENT APPLICATION NUMBER: US/09/668,096
CURRENT FILING DATE: 1980-09-01
PRIOR PLING DATE: 1989-09-01
PRIOR PLING DATE: 1989-09-01
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
SOFTWARE: Microsoft Office 97
SEC ID NOS: 12
SOFTWARE: Microsoft Office 97
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Matches:
Conservative:
Mismatches:
Indels:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 9, Application US/09668096
Patent No. 6312954
GENERAL INFORMATION:
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34.15%
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20.57%
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STATE: California
COUNTRY: United Sta
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
, ORGANISM: Oryza sativa
US-09-668-096-9
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Best Local Similarity:
Query Match:
DB:
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293

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NAME/KEY: misc_feature
| IOCATION: 1.4379
| OTHER INFORMATION: /note= "sequence = Arabidopsis |
| OTHER INFORMATION: thaliana API gene"
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION VUMBER: US/09/149,976
FILING DATE: 09-SEP-1998
CLASSIFICATION: 435
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                 PRIOR APPLICATION 1913.

PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 08/592,214

FILING DATE: 26-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 3291

TELEPHONE: (619) 535-9001

TELEPHONE: (619) 535-9001

TELEPHONE: (619) 535-904

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
FRATURE:
NAME/KEY: unsure
LOCATION: 2095..2098
OTHER INFORMATION: /note= "N = 0
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TYPE: nucleic acid
STRANDEDNESS: double
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Query Match:
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US-09-103-840A-2/c
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Patent No. 6127123
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identity
TITLE OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
ADDRESSEE: ADDRESSE
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NAME/KEY: misc_feature

LOCATION: 1..4379

OTHER INFORMATION: /note= "sequence = Arabidopsis

US-08-592-214A-17
       PatentIn Release #1.0, Version #1.25
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
FEATURE:
NAME/KEY: unsure
LOCATION: 2095..2098
OTHER INFORMATION: /note= "N = one or more
OTHER INFORMATION: nucleotides."
                                                                                                                                        CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1927
TELEPHONE: (619) 535-9901
TELEPHONE: (619) 535-9901
TELEPHONE: (619) 535-9901
TELEPKX: (619) 535-9901
                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,214A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.74%
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20.25%
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STATE: California
COUNTRY: United States
ZIP: 92122
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COMPUTER READABLE FORM:
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Best Local Similarity:
Query Match:
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1592 GGTTTTTGCAAACAAGGGAAACCAGCTTTAGCTTTTCCCTAAAACCAC-----TCTTAC 1645
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                                                                                                                                                                                                                                                                     36 GlyTyrPheGlnGlnTyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyr 55
                                                                                                                                      17 ---IleArgAlaAspSerSerGluGluLysArgHisArgLysArgLysLysHisHisArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09103840A

Batent No. 6294328

GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: PRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
1 MetLysilePheilePhevalPheileMetAlaLeuileLeuAlaMet-
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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09103840A

Sequence 1, Application US/09103840A

Patent No. 259432B

GENERAL INFORMATION:

APPLICANT: FLEISCHWAN, Robert D.

APPLICANT: WHITE, Owen R.

APPLICANT: VENTER, John C.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

TITLE OF INVENTION: TUBERCULGSIS

FILE REFERENCE: 24366-20007.00

CURRENT APPLICANTION NUMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

LENGTH: 4411529
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                                                                                                                                                                       OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                               ArgAlaAspSerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyr 37
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 PheGlnGlnTyrGlnProTyrGlnArgTyrPro
FILE REFERENCE: 24366-20007.00
CURRENY PELLING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3771669 CCGCCGGCGCCGTTCCCG 3771649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA

CRGANISM: Mycobacterium tuberculosis

CTHER INFORMATION: H37RV

US-09-103-840A-1
                                                                                                        TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 ProproAlaTyrProPhePro 58
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63.50
55.32%
36.17%
20.09%
                                                                                                                                                                                                                                                                            8.8e+05
63.50
55.32%
36.17%
20.09%
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Best Local Similarity:
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Best Local Similarity:
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Pred. No.:
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RESULT 12
US-09-359-301A-30
is Sequence 30, Application US/09359301A
is Sequence 30, Application US/09359301A
is Sequence 30, Application US/09359301A
is Sequence 30, Applications
is Applicant
is Applicant: Kumagai, Monto H.
is Applicant: McGee, David R.
is TITLE OF INVENTION: A DONOR PLANT INTO A DIFFERENT HOST PLANT IN AN ANTI-SENSE
is TITLE OF INVENTION: MCGEE, Mindows Version 3.0
is CURRENT PLING DATE: 1999-07-21
is NUMBER OF SEQ ID NOS: 42
is SOFTWARE: PastesEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                US-09-328-352-3819/c

US-09-328-352-3819/c

Sequence 3819, Application US/09328352

Patent No. 6562958

PRICENT NO. 6562958

PRICENT NEORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 3319
                            3779554 TACCGGCGGACGCGGCCTGCCGCGCGCGCCGCACCGCCATGGCCACCGCGTCA 3779496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 ITCAGGICIGCALCAGCACICGCAIAGAITITAITGGIACAGIAAAIAICAICAIAAGIA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 PhellephevalPhelleMetalaLeu-IleLeuAlaMetIleArgAlaAspSerSerGl 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37
-LeuAsnTyr
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444
8444
6444
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 rPheGlnGlnTyrGlnProTyrGlnArgTyrPro 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
   38 PheGlnGlnTyrGlnProTyrGlnArgTyrPro
                                                                                                                                                                             3779495 cceccecceccecciricce 3779475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 uGluLysArgHisArgLysArg----
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                                                                                                                   52 ProProAlaTyrProPhePro
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US-08-308-883-1
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PAGES:
DATE:
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DB:
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199 cagedatatcctcaacaagettatcctcagcaagatatcctccaccgtacgccctrcaa 258
                                                                                                                                                                                             35 ArgGlyTyrPheGlnGlnTyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAla 54
                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-06-308-808-81-1
US-06-308-808-1
Sequence 1, Application US/0830883
Sequence 1, INPORMATION:
REMERAL INPORMATION:
APPLICANT: Prieto, P. A.
APPLICANT: Baxter, J. H.
APPLICANT: Cummings, R.D.
TITLE OF INVENTION:
Method for Inhibition of Human Rotavirus Infection.
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPERATING SYSTEM: MacIntosh System 7.1
SOFTWARE: ClarisWorks 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,883
FILING DATE: 16-5EP-1994
FILING DATE: 16-5EP-1994
FILING DATE: 16-5EP-1994
FILING DATE: 16-5EP-1994
FILING APPLICATION DATA: No. 5576300 applicable
FELECOMMUNICATION INFORMATION:
TELEFAX: (614) 624-3774
TELEFAX: (614) 624-3774
TELEFAX: (614) 624-3774
TELEFAX: (614) 624-3774
TELEFAX: OST/63000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 DASE pairs
TYPE: MUCLE: Caid
STRANDEDNESS: Single
TOPOLOGY: Linear
                750
13
10
0
              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                       US-10-079-754A-10 (1-58) x US-09-359-301A-30 (1-750)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh System 7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human milk kappa-casein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Lonnie R. Drayer
ADDRESSEE: ROSS Products Division
ADDRESSEE: Abbott Laboratories
STREET: 625 Cleveland Avenue
CITY: Columbus
STATE: Ohio
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: Adult
HARLOTYRE:
TISSUE TYPE: Mammary gland
CELL TYPE:
CELL INFE:
                                                      58.33%
54.17%
19.94%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rxr: United States 43215
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FRAGMENT TYPE:
ORIGINAL SOURCE: Human
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                 259 TATCCTCCACCA 270
                                                                                                                                                                                                                                                                           55 TyrProPhePro 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
                                                                         Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESCRIPTION:
                                                      Percent Similarity:
Alignment Scores:
Pred. No.:
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UNITS:
VANE/KEY: CDS
LOCATION: 45...593
LOCATION: 45...593
LOCATION WITHOUD: DNA sequencing and restriction analysis
LOCATION THE encoded product of nucleotide SEQ ID NO: 1: is the human
OTHER INFORMATION:
AUTHORS: L. Hansson et al
TITLE: DNA Encoding Kappa-Casein, Process for Obtaining the Protein and Use They
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mukerji, P.
APPLICANT: Prieto, P.A.
APPLICANT: Seo, A. E.Y.
APPLICANT: Seo, A. E.Y.
APPLICANT: Cummings, R.D.
ADRESSEE: Lonnie R. Drayer
ADDRESSEE: Abbott indocate Division
ADDRESSEE: Abbott Laboratories
STREET: 625 Cleveland Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 ATGAAGAGTITICTICTAGTIGTCAAIGCCCTGGCAITAACCCTGCCTTTTTTGGCTGTG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetLysilePheilePhevalPhe---IleMetAlaLeuileLeuAlaMetIleArgAla 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 AspSerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyrPheGln 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 43215
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb storage (B) COMPUTER: Apple Macintosh
MEDIUM TYPE: 3.5 inch, 1.44 Mb storage (B) COMPUTER: Apple Macintosh
OPERATING SYSTEM: MacIntosh System 7.1(D) SOFTWARE: ClarisWorks 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 GlnTyrGlnProTyrGlnArgTyrProLeuAsnTyr---ProProAlaTyrProPhe 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                857
117
113
25
4
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-079-754A-10 (1-58) x US-08-308-883-1 (1-857)
ORGANELLE:
:MMEDIATE SOURCE: Human Mammary Gland
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOCUMENT NUMBER: PCT/W093/15196
FILING DATE: 25-DAN-1993
PUBLICATION DATE: 05-AUG-1993
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-730-163-1; Sequence 1, Application US/08730163; Sequence 1, Application US/08730163; Patent No. 5712250; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.7
63.00
50.85%
28.81%
19.94%
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                                                                  CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 625
TTTY: Columbus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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40 GlnTyrGlnProTyrGlnArgTyrProLeuAsnTyr---ProProAlaTyrProPhe 57
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Patent No. 622094

GENERAL INFORMATION:

APPLICANT: HANSSON, Lennart
APPLICANT: STROEMOVIST, Mats
APPLICANT: HERGSTROEM, Sven
APPLICANT: HERGSTROEM, Sven
APPLICANT: HERGSTROEM, Sven
APPLICANT: TOernell, Olle
APPLICANT: TOernell, Jan
TITLE OF INVENTION: OBTAINING THE PROTEIN AND USE THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPAGE: PATEMING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,799
FILING DATE: 06-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 88/92
PILING DATE: 23-JAN-1992
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HANSSON=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: HAN:
TELECOMMUNICATION INFORMATION:
TELEPHAN: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28,005
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SEQUENCE CHARACTERISTICS:
LENGTH: 857 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
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45..104
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45..593
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COUNTRY: USA
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NAME/KEY:
LOCATION:
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NAME/KEY:
LOCATION:
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LOCATION:
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NAME/KEY:
LOCATION:
FEATURE:
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; LOCATION:
US-08-256-799-1
                                                                                                                                                                         RESULT 15
US-08-256-799-1
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NAME/KEY: CDS
NAME/KEY: 45...593
LOCATION: 45...593
LDCATIFICATION: METHOD: DNA sequencing and restriction analysis
OTHER INFORMATION: The encoded product of nucleotide SEQ ID NO: 1: is the human
PUBLICATION INFORMATION:
AUTHORS: L. Hansson et al
AUTHORS: L. Hansson et al
TITLE: DNA Encoding Kappa-Casein, Process for Obtaining the Protein and Use The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 AIGAAGAGTITICTICTACIAGITGECAAIGCCCTGGCAITAACCCTGCCTTTTTTGCTGTG 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-079-754A-10 (1-58) x US-08-730-163-1 (1-857)
     CURRENT APPLICATION DATA:

'APPLICATION NUMBER: US/08/730,163
FILING DATE:
CLASSIFICATION: 435
RIOR APPLICATION DATA:
PELLING DATE: 16-SEP-1994
TELECOMMUNICATION INFORMATION:
TELEFAX: (614) 624-3774
TELEFAX: (614) 624-3774
TELEFX: (614) 624-3774
TELEFX: (814) 624-3774
TELEFX: (818) 624-3774
TELEFX: NO. 571-286
TENGTH: 857 base pairs
TYPE: NUCLeic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAPLOTYPE:
TISSUE TYPE: Mammary gland
CELL TYPE:
CELL LINE:
CRGANELLE:
IMMEDIATE SOURCE: Human Mammary Gland
CLONE:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOCUMENT NUMBER: PCT/W093/15196
; FILING DATE: 25-JAN-1993
; PUBLICATION DATE: 05-AUG-1993
; RELEVANT RESIDUES IN SEQ ID NO: US-08-730-163-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: Adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: No
ANTI-SENSE:
FRAGNENT TYPE:
ORIGINAL SOURCE: Human
ORCANISM: Homo sapiens
STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.7
63.00
50.85%
28.81%
19.94%
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CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
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113
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                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                   11.7
63.00
50.85%
28.81%
19.94%
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
Alignment Scores:
Pred. No.:
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Search completed: August 16, 2004, 00:49:11 Job time : 1484 secs

Title: Perfect score:

Run on:

Sequence:

Scoring table:

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WS-10-079-754A-15

Sequence 15, Application US/10079754A
Sequence 15, Application No. US2020164625A1
Sequence 15, Application No. US2020164625A1
SEQUENCE 15, Application No. US2020164625A1
SPELICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Dolenar, Adrian J.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Occopy 100.1068
CURRENT APPLICATION NUMBER: US/10/079,754A
CURRENT FILING DATE: 2002-02-19
FRICR FILING DATE: 2000-10-27
FRICR FILING DATE: 1999-10-29
FRICR APPLICATION NUMBER: US 60,162,701
FRICR FILING DATE: 12000-10-27
FRICR PILING DATE: 12000-08-22
FRICR PELING DATE: 1999-10-29
FRICR FILING DATE: 1000-08-22
FRICR FILING DATE: 1000-08-22
FRICR FILING DATE: 1000-08-23
NUMBER OF SEQ ID NOS: 15
67 14 US-10-079-754A-15
67 14 US-10-079-754A-16
15 14 US-10-079-754A-1
15 14 US-10-079-754A-1
15 14 US-10-079-754A-1
15 14 US-10-079-754A-1
16 US-10-079-754A-5
18 13 US-10-079-754A-5
19 US-10-128-714-2032
19 US-10-128-714-2032
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11 US-10-128-713-66
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14 US-10-128-716-72
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-MODBL=frame+ p2n. model - DEV=xlh
-MODBL=frame+ p2n. model - DEV=xlh
-MODBL=frame+ p2n. model - DEV=xlh
-Q-/ cgn2 1/USPTO spool/US10079754/runat_06082004_181230_29453/app_query.fasta_1.199
-DB=Published_Applications_NA - OFMT=fastap - SUFFTx=rnpb - MNNMATCH=0.1
-LCOPCL=0 - LOOFEXT=0 - UNITS=bits - STRAT=1 - END=-1 - MATRIX=blosum62
-TRANS=human40.cdi - LIST=45 - DOCALIGN=200 - THR_SCORE=pct - THR_MAX=100
-TRANS=human40.cdi - LIST=45 - DOCALIGN=200 - THR_SCORE=pct - THR_MAX=100
-THR_MIN=0 - ALIGN=15 - MODB=LOCAL - OUTFRT=-pto - NORM=ext - HEAPSIZE=500 - MINLEN=0
-MAXIEN=000000000 - USER=US10079754 @CGN 1 1 480 @runat 0608204 181230_29453
-NCPUS - LICPUS 3 - NO MMAP - LARGEQUERY - NG GCORES 0 - WAIT - DSPBLOCK=100
-LONGLOG - DEV TIMEOTT=120 - WARN TIMEOUT=30 - THRREADS=1 - CARAPOP=10 - XGAPEXT=0.5
-FGAPOP=6 - FGĀPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DBLOP=6 - DBLEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                          August 16, 2004, 00:23:24 ; Search time 326 Seconds (without alignments) 872.955 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/DFT_NEW PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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13: /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*
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19: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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316
1 MKIFIFVFIMALILAMIRAD......QQYQPYQRYPLNYPPAYPFP
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                   OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   3225727 segs, 2453303834 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                  BLOSUM62
Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Maximum DB seq length: 200000000
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Database :

Description

Query Match Length DB

Score

Result No.

Sequence 5, Appli Sequence 304, Appli Sequence 304, App Sequence 2032, Ap Sequence 6032, Ap Sequence 7032, Ap Sequence 5032, Ap Sequence 5032, Ap Sequence 89621, A Sequence 89621, A Sequence 89621, A Sequence 89621, A Sequence 313, App Sequence 313, App Sequence 66, Appli Sequence 1, Appli Sequence 86, Appli Sequence 1, Appli Sequence 86, Appli

Sequence 125, Sequence 2, P

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Sequence 4, Application US/10079754A Publication No. US20020164625A1 GENERAL INFORMATION:
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316.00
100.00%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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US-10-079-754A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                104 TCATCTGAAGAGAAACGTCACAGGAAACGGAAAAAACATCATAGAGGATATTTTCAACAA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 ATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGCCATGATTAGAGCTGAT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 TCATCTGAAGAAACGTCACAGGAAACGGAAAAAACATCATAGAGGATATTTTCAACAA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 SerSerGluGluLysArgHisArgLysArgLysLisHisArgGlyTyrPheGlnGln 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 200, Application US/10079623
; Sequence 200, Application WS/10079623
; Publication No. US20020169302A1
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Glenn, Matthew
; APPLICANT: Glenn, Matthew
; APPLICANT: Glenn, Matthew
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions isolated from bovine
; TITLE OF INVENTION: mammary gland and methods for their use;
; FILE REFERENCE: 11000, 1044623
; CURRENT APPLICATION NUMBER: US/10/079,623
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: PESESSEQ for Windows Version 4.0
; SEQ ID NO 200
LENGTH: 267
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 15 LENGTH: 267
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316.00
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316.00
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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ORGANISM: Bovine
                                                     TYPE: DNA
ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-079-623-200
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Pred. No.:
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DB:
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21 SerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyrPheGlnGln 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 TyrdlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyrProPhePro 58
Sequence 1, Application US/10079754A

Sequence 1, Application US/10079754A

Sequence 1, Application No. US20020164625A1

GENERAL INFORMATION:

APPLICANT: Glenn, Matthew

APPLICANT: Molenaar, Adrian J.

APPLICANT: Molenaar, Adrian J.

APPLICANT: Molenaar, Adrian J.

TITLE OF INVENTION: Compositions Isolated from Bovine

TITLE OF INVENTION: Compositions Isolated for Their US-

TITLE OF INVENTION: Mammary Gland and Methods for Their US-

TITLE OF INVENTION: Mammary Gland and Methods for Their US-

TITLE OF INVENTION: WOMBER: US-

TITLE OF INVENTION: DATE: 2002-02-19

PRIOR PILING DATE: 2006-10-27

PRIOR PILING DATE: 1999-10-29

PRIOR PILING DATE: 1999-10-23

PRIOR PILING DATE: 1999-10-23

PRIOR PILING DATE: 1999-08-23

MUMBER OF SEQ ID NOS: 15

SEQ ID NO 1

LENGTH: 505

TVDR: NANA
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APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Grigor, Murray R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
FILE REFERENCE: 11000.106
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 69/699,146
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR PILING DATE: 1999-10-29
PRIOR PILING DATE: 1999-10-29
PRIOR PILING DATE: US 60,162,701
PRIOR PILING DATE: US 60,150,330
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Matches:
Conservative:
Mismatches:
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149 ATGAAGATCTTTATCTTTATCTTCATTATGGCTCTCATCCTAGCCATGATTAGAGCTGAT 208
                                                          41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyrProPhePro 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277.00
82.61%
82.61%
87.66%
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Best Local Similarity: 8
Query Match: 6
DB:
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ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                        41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyrProPhePro 58
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| Sequence 2. Application Wo. US20020164625A1
| Publication No. US20020164625A1
| GENERAL INFORMATION:
| APPLICANT: Glenn, Matthew
| APPLICANT: Glenn, Matthew
| APPLICANT: Glenn, Matthew R. APPLICANT: Deprive, Murray R. APPLICANT: Davis, Stephen R. TITLE OF INVENTION: Compositions Isolated from Bovine TITLE OF INVENTION: Mammary Gland and Methods for Their USE TITLE OF INVENTION: Mammary Gland and Methods for Their USE TITLE OF INVENTION: MAMBER: US 100.006 B CURRENT APPLICATION NUMBER: US 2002-02-19
| PRIOR PELING DATE: 2000-10-27
| PRIOR PELING DATE: 1999-10-29
| PRIOR PELING DATE: 1999-10-29
| PRIOR PELING DATE: 1999-10-29
| PRIOR PELING DATE: 2000-06-22
| PRIOR PELING DATE: 1999-10-29
| PRIOR FILING DATE: 2000-06-22
| PRIOR FILING DATE: 1999-10-23
| NUMBER OF SEQ ID NOS: 15
| SEQ ID NO 2
| LENGTH 1: 585
                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                 US-10-079-754A-10 (1-58) x US-10-079-754A-4 (1-604)
         ; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15
; SCOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Bovine
US-10-079-754A-4
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315.00
100.00%
98.28%
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316.00
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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; ORGANISM: Bovine
US-10-079-754A-2
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Pred. No.:
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US-10-079-754A-6

US-10-079-754A-6

US-10-079-754A-6

Sequence 6, Application US/10079754A

Publication No. US20020164625A1

GENERAL INFORMATION:

APPLICANT: Glenn, Matthew

APPLICANT: Glenn, Matthew

APPLICANT: Glenn, Marmary R.

APPLICANT: Molenaar, Adrian J.

TITLE OF INVENTION: Compositions Isolated from Bovine

TITLE REFERENCE: 11000.1068

CURRENT APPLICATION NUMBER: US/10/079,754A

CURRENT FILING DATE: 2000-10-27

PRIOR FILING DATE: 2000-10-29

PRIOR FILING DATE: 2000-10-29

PRIOR FILING DATE: 2000-08-22

PRIOR FILING DATE: 2000-08-22

PRIOR FILING DATE: 2000-08-22

PRIOR FILING DATE: 1999-08-23

NUMBER OF SEQ ID NOS: 118

SOFTWARE: FastSEQ for Windows Version 4.0

SERVICENT: FRENCHM: CPE
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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APPLICANT: Glam, Mathew APPLICANT: Grigor, Murray R.
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us-10-079-754a-10_1.rnpb

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; TYPE: DNA
; ORGANISM: Bovine
US-10-079-754A-5
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     SEQ ID NO 5
LENGTH: 96
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APPLICANT: Molenaar, Adrian J.

APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
FILE REPRENCE: 11000.1668
CURRENT APPLICATION NUMBER: US/10/079,754A
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 09/699,146
PRIOR APPLICATION NUMBER: US 09/699,146
PRIOR APPLICATION NUMBER: US 00.162,701
PRIOR APPLICATION NUMBER: US 09/644,190
PRIOR APPLICATION NUMBER: US 09/644,190
PRIOR FILING DATE: 1999-08-22
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
FILE REPERENCE: 11000.1068
CURRENT APPLICATION NUMBER: US/10/079,754A
CURRENT PILING DATE: 2002-02-19
FRIOR PPLING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR PLING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR APPLICATION NUMBER: US 60,164,190
PRIOR FILING DATE: 1999-08-22
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
Conservative:
Mismatches:
Indels:
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55.13%
52.56%
53.96%
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Best Local Similarity:
Query Match:
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ORGANISM: Bovine
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Pred. No.:
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APPLICANT: Malyankar, Uriel
APPLICANT: MacDougall, John
APPLICANT: MacDougall, John
APPLICANT: Store, David
APPLICANT: Lepley, Denise et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODE FILE REFERENCE: 21402-416 A
CURRENT APPLICATION NUMBER: US/10/210,172
CURRENT FILING DATE: 2001-08-01
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                                                                                                                                                                                           38 PheGlnGlnTyrGlnProTyrGlnArgTyrProLeuAsnTyrProFroAlaTyrPro
    96
118
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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PRIOR PELING DATE: 2001-08-01

PRIOR PILING DATE: 2001-08-02

PRIOR FILING DATE: 2001-08-02

PRIOR FILING DATE: 2001-09-31

PRIOR APPLICATION NUMBER: 60/373,814

PRIOR APPLICATION NUMBER: 60/373,814

PRIOR PILING DATE: 2001-09-13

PRIOR FILING DATE: 2001-08-03

PRIOR FILING DATE: 2001-08-03

PRIOR PILING DATE: 2001-08-03

PRIOR APPLICATION NUMBER: 60/310,291

PRIOR FILING DATE: 2001-08-08

PRIOR PILING DATE: 2001-08-08

PRIOR FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                           Sequence 167, Application US/10210172 Publication No. US20040043928A1 GENERAL INFORMATION:
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FILING DATE: 2001-08-07
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Ji, Weizhen
Padigaru, Muralidhara
Casman, Stacie
Voss, Edward
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles
APPLICANT: Patturajan, Meera
APPLICANT: Pena, Carol
APPLICANT: Rieger, Daniel
APPLICANT: Shimkets, Richard
APPLICANT: Zerhusen, Bryan
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Rastelli, Luca
Spytek, Kimberly
Edinger, Shlomit
                        112.00
100.00%
94.74%
35.44%
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Hjalt, Tord
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Vernet, Corine
Anderson, David
Guo, Xiaojia
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Gorman, Linda
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                                 Percent Similarity:
Best Local Similarity:
Query Match:
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PRIOR APPLICATION NUMBER: 60/311,979
PRIOR PILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 60/313,201
PRIOR PILING DATE: 2001-08-17
PRIOR PILING DATE: 2001-08-17
PRIOR PILING DATE: 2001-08-16
Remaining Prior Application data removed - See File Wrapper or PALM.
SOFTWARE: CuraSequist version 0.1
ENGTH: 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      387 TATCAGCCAGTTCCAGAACAACCACTA---TACCCACAACCATAC 428
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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61.82%
49.09%
34.81%
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110.00
61:82%
49.09%
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ORGANISM: Homo sapiens
                                                                                                                                                                                  FEATURE:

, NAME/KEY: CDS

, LOCATION: (270)..(455)

US-10-210-172-167
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Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
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Pred. No.:
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84 AIGAAGITITITGICITITGCTITAGICITITGCTCTCAIGAITITCCAIGAITAGCGCIGAI 143
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21 SerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyrPheGlnGln 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INCRAMILLOW:
APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.U34.DIV
CURRENT APPLICATION NUMBER: US/09/992,600A
CURRENT APPLICATION NUMBER: US/09/924,340
PRIOR FILING DATE: 2001-01-03
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-15
PRIOR PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-06-15
PRIOR 
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Mismatches:
Indels:
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Matches:
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94.50
56.36%
32.73%
29.91%
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LOCATION: 84.317
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 318..438
FEATURE:
NAME/KEY: POLYA signal
LOCATION: 397..402
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Best Local Similarity:
Query Match:
DB:
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LOCATION: 1..83
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41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyr 55

CURRENT APPLICATION NUMBER: US/09/992,095B

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APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.USS.DIV
Sequence 5, Application US/09992095B Publication No. US20030157485A1 GENERAL INFORMATION:
                                                                                     US-09-992-095B-5
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84 ATGAAGTTTTTTGTCTTTGCTTTAGTCTTTGGCTCTCATGATTTCCATGATTAGCGCTGAT 143
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Publication No. US2030170628A1
GENERAL INFORMATION:
APPLICANT: Benjain, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: G-091US08DIV
CURRENT APPLICATION NUMBER: US/09/999,570
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-08-06
PRIOR PLILNG DATE: 2001-08-06
PRIOR PLILNG DATE: 2001-08-06
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION WUMBER: US 09/924,340
PRIOR APPLICATION WUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR PLILING DATE: 2001-06-29
PRIOR PLILING DATE: 2001-06-29
PRIOR APPLICATION WUMBER: US 60/298,698
PRIOR APPLICATION WUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-05-26
NUMBER OF SEQ ID NOS: 112
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.50
56.36%
32.73%
29.91%
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; LOCATION: 423..438
US-09-992-095B-5
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LOCATION: 84..317
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NAME/KEY: 3'UTR
LOCATION: 318..43
FEATURE:
NAME/KEY: polyA s
LOCATION: 397..4
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LOCATION: 1..83
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DB:
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                                                                                             US-09-924-340-5
Sequence 5, Application US/09924340
Publication No. US20030027248A1
GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
TILE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
TILE REFERENCE: 91.U32.REG
CURRANT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-05-25
SOFTWARE: JBatent
SSOFTWARE: JBatent
                       186 ---GAAAAGCATCATTCATACCATATCACCACTACTACCACTTTTT 227
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Mismatches:
Indels:
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Matches:
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0.000281 94.50 56.36% 32.73% 29.91%

Alignment Scores:

Percent Similarity: Best Local Similarity:

Query Match:

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polyA signal

318..438

NAME/KEY: 5'UTR LOCATION: 1..83 NAME/KEY: 84..317 NAME/KEY: 3'UTR LOCATION: 318..43 NAME/KEY: 901YA

LOCATION: 397..... LOCATION: 397.... NAME/KEY: polyA site

; LOCATION: 4: US-09-924-340-5

TYPE: DNA ORGANISM: Homo sapiens

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84 AIGAAGITITIGICTITIGCTITIAGICITIGCTCTCAIGAITITCCAIGAITAGCGCIGAI 143
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; Publication No. US20303092011A1
; GENERAL INFORMATION:
APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US6.DIV
CURRENT APPLICATION NUMBER: US/10/000,489
; CURRENT APPLICATION NUMBER: US/924,340
; PRIOR FILING DATE: 2001-11-14
; PRIOR PLING DATE: 2001-08-06
; PRIOR FILING DATE: 2001-08-06
; PRIOR FILING DATE: 2001-08-06
; PRIOR FILING DATE: 2001-03-06
; PRIOR FILING DATE: 2001-08-06
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777
138
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Matches:
Conservative:
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PRIOR FILING DATE: 2001-08-06

PRIOR APPLICATION NUMBER: US 60/305,456

PRIOR APPLICATION NUMBER: US 60/302,277

PRIOR PELING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: US 60/298,574

PRIOR APPLICATION NUMBER: US 60/293,574

PRIOR APPLICATION NUMBER: US 60/293,574

SOFTWARE: JPatent

SEQ ID NO 5

LENGTH: 438
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94.50
56.36%
32.73%
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NAME/KEY: polyA signal
LOCATION: 397..402
FEATURE:
                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       // NAME/KEY: polyA site
// LOCATION: 423..438
US-09-999-570-5
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: CDS
LOCATION: 84..317
FEATURE:
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LOCATION: 318..438
                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..83
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Pred. No.:
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US-10-000-489-5
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Search completed: August 16, 2004, 01:12:54 Job time : 331 secs

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21 SerSerGluGluLysArgHisArgLysArgLysHisHisArgGlyTyrPheGlnGln 40
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: UPatent
SEQ ID NO 5
LENGTH: 438
                                                                                                                                                                                                                                                                                                                                                                    94.50
56.36%
32.73%
29.91%
                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..83
NAME/KEY: CDS
LOCATION: 84..317
NAME/KEY: 9'UTR
LOCATION: 318..438
NAME/KEY: polyA_signal
LOCATION: 397..402
NAME/KEY: polyA_site
LOCATION: 423..438
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Best Local Similarity:
Query Match:
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Pred. No.:
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RESULT 1
US-08-602-999A-268
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Sequence 268, App
Sequence 35, App
Sequence 376, App
Sequence 376, App
Sequence 3551, App
Sequence 4214, App
Sequence 5885, App
Sequence 8060, App
Sequence 3062, App
Sequence 3062, App
Sequence 3062, App
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25, Appi
25, Appi
8756, Ap
97, Appi
167, App
6490, Ap
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10559, A
4390, Ap
4, Appli
                                                                                              August 6, 2004, 17:06:10 ; Search time 18 Seconds (without alignments) 166.350 Million cell updates/sec
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1. /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

3. /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

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5. /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

5. /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-500-124-268
US-09-610-384-35
US-09-198-452A-1200
US-09-634-238-376
US-09-134-000C-3551
US-09-134-000C-3551
US-09-134-001C-3650
US-09-134-6810-6400
US-09-134-6810-6400
US-09-134-6810-6400
US-09-134-6810-6400
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US-09-489-039A-10559
US-09-134-001C-4390
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US-09-540-236-1934
US-09-252-991A-29893
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                                                                                                                                                                                                                                                                                  389414 segs, 51625971 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Listing first 45 summaries
                                                                - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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58
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                                                                                                                                                                                   0
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Perfect score:
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ALIGNMENTS

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US-UG-LOW-NUMBER OF A ADDICATION US/0860299A

SEQUENCE OF ADDICATION:
GENERAL INCORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: THORN Judith M.
APPLICANT: THORN Judith M.
APPLICANT: THORN JUDILIAN, LAWNERCE A.
APPLICANT: FOWLKES, Dana M.
APPLICANT: STORES:
CONFURER READABLE FORM:
MODIUM TYPE: FLOPPY disk.
COMPUTER: The PC COMPUTED M.
COMPUTER: THE PC COMPUTED M.
APPLICANT ON NUMBER: US/08/602,999A
FILING DATE: 116-FEB-1996
CLASSIFFATION NUMBER: US/08/602,999A
FILING DATE: 116-FEB-1996
THELEPHONE: 12 amino acid
TELESPHONE: 12 amino acid
TELESPHONE: ACID NO: 268:
SEQUENCE CHARACTERISTICS:
THELEPHONE: 12 amino acid
TYPE: OCOUNTY TO OCON TO OC
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10.3%; Score 6; DB 4; Length 103;
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                                                                                                                                                                                                          Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-7261
                                                                                                                                                                                                                                                                  22 SEEKRH 27
                                                                                                                                                                                                                                                                                                  86 SEEKRH 91
                                                                                                     LENGTH: 95
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                                                                                                                                                                                         APPLICANT: SPACE, ANGLEW D.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWIKES, Dana M.
APPLICANT: RIDER, James B.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.3%; Score 6; DB 4; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Pred. No. 6.6
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIPTCATION
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 16-FEB-1996
ATTONEY/AGENT INFORMATION:
NAME: Misrock, S. Leelie
REGISTRATION NUMBER: 18,872
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7261, Application US/09621976
Patent No. 6639063
                                                                                                                      Sequence 268, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 268:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.08;
                                                                                                                                                                                Andrew B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 amino acids
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Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jobert, S. APPLICANT: Giordano, J.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & 1
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51 YPPAYP 56
                                                                                                                                                                                   SPARKS
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                                    1 YPPAYP 6
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US-09-621-976-7261
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                                                                                                             JS-09-500-124-268
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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JAMESON, Brad
TEPPER, Mark
TITLE OF INVENTION: CD28/CTLA-4 INHIBITING PEPTIDOMIMETICS,
PHARMACEUTICAL COMPOSITIONS THEREOF, AND METHOD OF USING
SAME
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                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                         Length 95;
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COUNTRY: U.S.A.
ZIP: 20001
ZIP: 20001
COMPUTEN: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTEN: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: RC-DOS/MS-DOS
OPERATING RELEGASE #1.0, Version #1.30
TITLE OF INVENTION: ESTS and Encoded Human Proteins. FILE REFERENCE: GENSAT. 0549F2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 7261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSER: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninch Street N.W., Ste. 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/460,384
FILING DATE: 13-Dec-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/12312
FILING DATE: 11-JUN-1998
APPLICATION NUMBER: US 60/049,470
FILING DATE: 12-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: YUN, Allen C
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: EL TAYAR=1A
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                        Score 6; Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT. 4
US-09-460-384-35
US-09-460-384-35
Sequence 35, Application US/09460384;
Patent No. 6337316
GENERAL INFORMATION:
APPLICANT: EL TAYAR, Nabil
APPLICANT: BLECHNER, Steven
                                                                                                                                                                                                                                                        10.3%; Scc.
100.0%; Pre
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INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 103 amino acids
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Sequence 4214, Application US/09543681A

| Sequence 4214, Application US/09543681A
| Sequence 4214, Application US/09543681A
| Sequence 4214, Application
| Application NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
| TITLE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS
| TITLE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS
| TITLE OF INVENTION: UNCOREACE US/09/543,681A
| CURRENT APPLICATION NUMBER: US/09/543,681A
| CURRENT PILING DATE: 2000-04-05
| PRIOR FILING DATE: 1999-04-09
| NUMBER OF SEQ ID NOS: 8344
                        Sequence 7386, Application US/09489039A

Batent No. 6610836
GENERAL INFORMATION
OF 6610836
GENERAL INFORMATION
OF 6610836
GENERAL INFORMATION
OF 6610836
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US/0117,747
PRIOR APPLICATION NUMBER: US/0117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7386
INDICTH: 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3551, Application US/09134000C

Batent No. 6617156

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENITION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENITION: NUCLEIC ACID AND THERAPEUTICS
FILE REPERBRÜCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1999-08-15
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR PILING DATE: 1999-08-15
NUMBER OF SEC ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 3551
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 146;
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100.0%; Pred. No. 50;
iive 0; Mismatches
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100.0%; Pred. No. 55;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 6; Conservative
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US-09-134-000C-3551
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US-09-134-000C-3551
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                          Gaps
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Lubbers, Mark W.
Lubbers, Mark W.
Lucant: Dekker, James
APPLICANT: Christensson, Anna C.
APPLICANT: Holland, Ross
APPLICANT: Wolde, Paul W.
APPLICANT: Reid, Julian R.
APPLICANT: Coolbear, Timothy
TITLE OF INVENTION: them and methods for using them.
FILE REPERENCE: 11000.1043 ut
FILE REPERENCE: 11000.1043 ut
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWARE: FastSEQ for Window-
SEQ ID NO 376
LYPE: PP"

LYPE: PP"

TYPE: PP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                          .;
0
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100.0%; Pred. No. 39;
Live 0; Mismatches
    ; Pred. No. 38;
0; Mismatches
                                                                                                                                                                                                       Sequence 1200, Application US/09198452A Patent No. 6559294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Lactobacillus rhamnosus US-09-634-238-376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1200
100.08;
    Best Local Similarity 100.8
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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                                                                  39 QQYQPY 44
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US-09-198-452A-1200
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GENERAL INFORMATION:
APPLICANT: GARY BRETON:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL:)
TITLE OF INVENTION: UDIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION MUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR RILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
SEQ ID NOS: 8344
LENGIH: 298
    Sequence 3065, Application US/09134001C

Sequence 3065, Application US/09134001C

Sequence 3065, Application US/09134001C

Sequence 3065, Application US/09134001C

SENERAL INFORMATION:

APPLICANT: Lyan Doucette-Stamm et al

APPLICANT: BETERRACE: GTC-007

FILE REPERRACE: GTC-007

FILE REPERRACE: GTC-007

FILE REPERRACE: GTC-007

FILE REPERRACE: GTC-007

FRICK APPLICATION NUMBER: US 60/064,964

PRICK PILING DATE: 1997-11-08

PRICK FILING DATE: 1997-11-08

NUMBER: OF SEQ ID NOS: 5674

SEQ ID NO 3062

LENGTH: 263
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APPLICANT: RECIO-PINTO, ESPERANZA
TITLE OF INVENTION: VOLTAGE GATED SODIUM CHANNELS FROM
TITLE OF INVENTION: HUMAN PERIPHERAL NERVE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
STREET: CLINTON SQUARE, P.O. BOX 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.3%; Score 6; DB 4;
100.0%; Pred. No. 81;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.3%; Score 6; DB 4;
100.0%; Pred. No. 90;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-543-681A-5642
; Sequence 5642, Application US/09543681A
; Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Proteus mirabilis US-09-543-681A-5642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10,3
Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                               Sequence 5.55, Application US/09543681A

Sequence 6.65709

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 5885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8060, Application US/09489039A

Sequence 8060, Application US/09489039A

Patent No. 6610836

Patent No. 6610836

Patent No. 6610836

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CURRENT APPLICATION: NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US/00/01-27

FRIOR FILING DATE: 1999-01-29

PRIOR FILING DATE: 1999-01-29

SEQ ID NO 8060

LENGTH: 241
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                                                                                                                     Length 201;
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o. 76;
                                                                                                                     Score 6; DB 4;
Pred. No. 65;
                                                                                                        10.3%; Scor.
100.0%; Pred. No. v.
0; Mismatches
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100.0%; Pred. No. 76;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT; ORGANISM: Proteus mirabilis
US-09-543-681A-5885
                  LENGTH: 201
TYPE: PRT
ORGANISM: Proteus mirabilis
                                                                                                        Query Match
Best Local Similarity 100.
دروا 6، Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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US-09-489-039A-8060
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US-09-543-681A-5885
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                                                                                 US-09-543-681A-4214
SEQ ID NO 4214
LENGTH: 201
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Sequence 25, Application US/09097889

Patent No. 6218117

GENERAL INFORMATION:
APPLICANT: Herinstadt, Corrina
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: AGENTS THAT QUANTATIVELY ALTER DETECTABLE
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
COUNTRY: Seattle
STATE
STAT
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                                                                                                         CONDITY: USA
CIDITAT: USA
CIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CHRRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/605,284B
FILING DATE: 09-FEB-1996
CLASSIFICATION: 424
ATTORNEY FAGENT INFORMATION:
NAME: BRAWAN, SUSAN J.
REGISTRATION NUMBER: 19603/800 (CRF D-1705)
THIECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1606
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: ATRANDEDNESS: not relevant
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,889
FILING DATE: 15-JUN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROSENMAN Ph.D. Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 660088.417
TELECOMMUNICATION INFORMATION:
TELETERMONE: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
10.3%; Score 6; DB 3;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches
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MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
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                                               NEW YORK
ROCHESTER
                                                                                      USA
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US-09-097-889-25
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| INFORMATION FOR SEQ ID NO: 25:
| SEQUENCE CHRACTERISTICS:
| ILENGTH: 380 amino acids | TYPE: amino acid |
| TYPE: amino acid | TYPE: amino acid |
| TYPE:
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August 6, 2004, 17:09:05 ; Search time 46 Seconds (without alignments) 395.513 Million cell updates/sec
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58
1 MKIFIFVFIMALILAMIRAD......QQYQPYQRYPLNYPPAXPFP
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/ cgn2_6/prodata/2/pubpaa/USO9A_PUBCOMB.pep:*
/ cgn2_6/prodata/2/pubpaa/USO9G_PUBCOMB.pep:*
/ cgn2_6/prodata/2/pubpaa/USO9C_PUBCOMB.pep:*
/ cgn2_6/prodata/2/pubpaa/USO9_MEW_PUB.pep:*
/ cgn2_6/prodata/2/pubpaa/USO0A_PUBCOMB.pep:*
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/ cgn2_6/ptodata/2/pubgaa/USO8_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 7, Appli	Sequence 10, Appl	Sequence 8, Appli	Seguence 12, Appl	Seguence 9, Appli	Sequence 11, Appl	Sequence 70822, A	Seguence 586, App	Sequence 168, App	Sequence 145633,	Sequence 257786,	Sequence 1, Appli	Sequence 268, App	Sequence 170, App	Sequence 164611,
ΩI	US-10-079-754A-7	US-10-079-754A-10	US-10-079-754A-8	US-10-079-754A-12	US-10-079-754A-9	US-10-079-754A-11	US-10-425-114-70822	US-09-876-904A-586	US-10-210-172-168	US-10-424-599-145633	US-10-424-599-257786	US-09-927-436-1	US-10-161-791-268	US-10-210-172-170	US-10-424-599-164611
DB	13	13	13	13	13	13	12	10	12	12	12	0	14	12	12
a Query Match Length DB	58	58	28	59	70	21	363	13	62	72	150	12	12	47	52
% Query Match	100.0	100.0	87.9	58.6	46.6	19.0	13.8	12.1	12.1	12.1	12.1	10.3	10.3	10.3	10.3
Score	58	58	51	34	27	11	80	7	7	7	7	9	φ	9	9
Result No.	1	7	m	4	Ŋ	9	7	80	6	10	11	12	13	14	15

Seguence 774, App				15679	Sequence 221250,	Sequence 250830,	Sequence 178932,	Sequence 47763, A	Sequence 225829,	Sequence 169059,	266	Sequence 791, App	Sequence 224333,	Sequence 1200, Ap	6237,	Sequence 234852,	27934	19741	21609	14591		edneuce	Sequence 205, App	Sequence 159623,	Seguence 159963,	20348	Sequence 279792,	Sequence 2076, Ap	Sequence 200341,
US-09-864-408A-774	4-599	5-258-5	5-258-6	US-10-424-599-156798	4-599-22125	US-10-424-599-250830	7-9	-761-477	3-10-424-	US-10-424-599-169059	4-	3-5	4-5	9	-63	4-599-23485	0-424-599-	1-424-599-19741	4-599-21	0-424-599-1	0-437-963-1	0-282-122A-	0-001	0-424-	0-424-599	0-424-	0-424-599-		US-10-437-963-200341
11	12	14	14	12	12	12	16	σ	12	12	12	디	12	15	σ	12	12	12	12	12	16	12	13	12	12	12	12	16	16
26	62	63	63	71	71	71	72	75	81	96	99	106	107	107	108	110	113	114	117	119	125	126	130	144	153	161	161	161	161
10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3			10.3										
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16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	3.4	35	36	37	38	თო	40	41	42	43	44	45

ALIGNMENTS

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Sequence 12, Application US/10079754A Publication No. US20020164625A1 GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Bovine
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ORGANISM: Bovine
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                                                                                                                                   APPLICANT: Glenn, Mattnew
APPLICANT: Glenn, Mattnew
APPLICANT: Glegor, Murray R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Compositions Isolated from Bovine
FILE REFERENCE: 11000.1068
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 09/699,146
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 1999-06-23
PRIOR FILING DATE: 1999-06-23
PRIOR FILING DATE: 1999-06-23
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Grigor, Marray R.
APPLICANT: Grigor, Marray R.
APPLICANT: Grigor, Marray R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
CURRENT PELICATION NUMBER: US/10/079,754A
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 09/699,146
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: US 60,150,330
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 100.0%; Score 58; DB 13; Length 58; 1 Similarity 100.0%; Pred. No. 6.9e-53; 58; Conservative 0; Mismatches 0; Indels
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llarity 100.0%; Pred. No. 1.4e-45;
Conservative 0; Mismatches 0;
                                            Sequence 10, Application US/10079754A Publication No. US20020164625A1 GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/10079754A Publication No. US20020164625A1 GENERAL INFORMATION:
APPLICANT: Glenn, Mathew APPLICANT: Grigor, Murray R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 51; Conservat
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Best Local Similarity
Matches 58; Conserv
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ORGANISM: Bovine
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8 FIMALILAMIRADSSEEKRHRKRKKKHHRGYFQQYQPYQRYPLNYPPAYPFP 58
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APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Bavis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
FILE REPERSURE: 11000.1068
CURRENT APPLICATION NUMBER: US/10/079,754A
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR FILING DATE: 12000-10-27
PRIOR FILING DATE: 12000-09-22
PRIOR FILING DATE: 12000-09-22
PRIOR FILING DATE: 1209-10-29
PRIOR FILING DATE: 1099-10-29
PRIOR FILING DATE: 1099-10-28
PRIOR FILING DATE: 1099-10-28
PRIOR FILING DATE: 1099-10-28
PRIOR FILING DATE: 1099-10-28
PRIOR PLING DATE: 1099-10-28
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APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
TITLE OF INVENTION: MAMBER: US/10/079,754A
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 09/699,146
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR APPLICATION NUMBER: US 09/644,190
PRIOR FILING DATE: 1999-08-22
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SEQ ID NOS: 15
SEQ ID NO 12
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Hjalt, Tord
Rastelli, Luca
Spytek, Kimberly
Edinger, Shlomit
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Guo, Xiaojia
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Gorman, Linda
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                                                        Query Match 13.8
Best Local Similarity 100.
Matches 8; Conservative
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Gerlach, Va.
Tord
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Best Local Similarity
Matches 7; Conserv
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US-10-425-114-70822
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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Sequence 70822, Application No US20040034888A1

Publication No US2004003488BA1

APPLICANT: Liu, Jingdong

APPLICANT: Taboaka, Jack E

APPLICANT: ApplicANT: Aboaka, Jack E

APPLICANT: Gao, Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

SEQ ID NO 70822

LEG THE TRIANG DATE: ADDITED TO THE TRIANG DATE: ADDIT
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APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
FILE REFERENCE: 11000.1068
CURRENT FILING DATE: 2002-19
PRIOR APPLICATION NUMBER: US/10/079,754A
CURRENT FILING DATE: 2002-19
PRIOR APPLICATION NUMBER: US 09/699,146
PRIOR APPLICATION NUMBER: US 09/699,146
PRIOR APPLICATION NUMBER: US 09/644,190
PRIOR PILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
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                                                            Query Match 46.6%; Score 27; DB 13; Length 70; Best Local Similarity 100.0%; Pred. No. 1.6e-20; Matches 27; Conservative 0; Mismatches 0; Indels
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ORGANISM: Zea mays
PERATURE:
OTHER INFORMATION: Clone ID: UC-ZMFLB73150C02_FLI.pep
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100.0%; Pred. No. 0.00027;
iive 0; Mismatches 0;
                                                                                                                                                                                              8 FIMALILAMIRADSSEEKRHRKRKKHH 34
                                                                                                                                                                                                                                                 8 FIMALILAMIRADSSEEKRHRKRKKHH 34
                                                                                                                                                                                                                                                                                                                                                                                US-10-079-754A-11
; Sequence 11, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 19.0
Best Local Similarity 100.
Matches 11; Conservative
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ORGANISM: Bovine
          US-10-079-754A-9
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Sequence 586, Application US/09876904A

Sequence 586, Application No. US20030072794A1

Publication No. US20030072794A1

GENERAL INFORMATION:
TITLE OF UNVENTION: ENCASSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

TITLE OF INVENTION: CONUCGATES INTO TARGETED LIPOSOME COMPLEXES

CURRENT PILING DATE: 2001-06-08

PRIOR FILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 629

SOFTMANE: PATENT VET. 2.1

SEQ ID NO S86

LENGTH: 13
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0
Length 363;
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13.8%; Score 8; DB 12; 100.0%; Pred. No. 4.4;
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100.0%; Pred. No. 2.6
tive 0; Mismatches
                                                   0; Mismatches
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Publication No. US20040043928A1
GENERAL INFORMATION:
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Ji, Weizhen
Padigaru, Muralidhara
Casman, Stecie
Voss, Edward
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APPLICANT: Miller, Charles
APPLICANT: Patturajan, Merra
APPLICANT: Pena, Carol
APPLICANT: Rieger, Daniel
APPLICANT: Shimkets, Richard
APPLICANT: Zerhusen, Bryan
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Sou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBNCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 257786
LENGTH: 150
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1 Sequence 1, Application US/09927436

2 Sequence 1, Application US/09927436

3 Patent No. US2002015455A1

5 Patent No. US2002015455A1

5 APPLICANT: Tadayoni-Rebek, Mitra

3 APPLICANT: Amshey, Joseph W.

4 APPLICANT: Amshey, Joseph W.

5 TILLE OF INVENTION: Highly Homogeneous Molecular Markers for Electrophoresis

7 TILLE OF INVENTION: Highly Homogeneous Molecular Markers for Electrophoresis

7 TILLE OF INVENTION: Highly Homogeneous Molecular Markers for Electrophoresis

7 CURRENT APPLICATION NUMBER: US/09/927,436

7 CURRENT FILING DATE: 2001-08-13

7 PRIOR FILING DATE: 2000-08-11

7 NUMBER OF SEQ ID NOS: 10

7 SEQTWARE: Patentin version 3:0

7 EENGTH: 12
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_74804C.1.pep
US-10-424-599-257786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (1)..(150)
OTHER INFORMATION: unsure at all Xaa locations
FRATURE:
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CTHER INFORMATION: Synthetic peptide
NAME/KEY: MOD RES
COCATION: (2) - (2)
COTHER INFORMATION: Modified with fluorescein
NAME/KEY: MOD RES
LOCATION: (5) - (5)
COTHER INFORMATION: Modified with fluorescein
US-09-927-436-1
0; Mismatches
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Publication No. US20040031072A1
GENERAL INFORMATION:
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7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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   Matches
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          APPLICANY: ELEBERANC, Usie
APPLICANY: Malyankar, Urie
APPLICANY: Alsobrook II, John
APPLICANY: Alsobrook II, John
APPLICANY: Labelby, Denise et al.
APPLICANY: AND APPLICANION NUMBER: 60/309,501
APRIOR FILING DATE: 2001-08-01
APPLICANY: APPLICANION NUMBER: 60/310,991
APPLICANY: APPLICANION NUMBER: 60/310,991
APPLICANY: APPLICANION NUMBER: 60/310,991
APPLICANY: APPLICANION NUMBER: 60/310,991
APPLICANY: APPLICANION NUMBER: 60/311,292
APPLICANY: APPLICANION NUMBER: 60/311,292
APPLICANY: APPLICANION NUMBER: 60/312,992
APPLICANY: APPLICANION NUMBER: 60/312,993
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APPLICANY: APPLICANION NUMBER: 60/312,993
APPLICANY: APPLICANION NUMBER: 60/312,993
APPLICANION NUMBER: 60/312,993
APPLICANY: APPLICANION NUMBER: 60/3
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Sequence 145633, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPRENCE: 38-21(53223)

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 145633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.1%; Score 7; DB 12; Length 72; 100.0%; Pred. No. 12;
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US-10-424-599-145633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 12.1%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 ADSSEEK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADSSEEK 25
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Best Local Similarity
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20 DSSEEK 25
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                                         Gaps
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0
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APPLICANT: KNY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: DUTLIAM, Lawrence A.
APPLICANT: FOWLKES, Dana M.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James B.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: ISOLATING AND USING SAME NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York.
CHARLES AND MENTION: MAN WORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 14; Length 12;
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                                         0; Indels
  Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: FIDOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRICE APPLICATION:
APPLICATION:
APPLICATION:
Query Match 10.3%; Score 6; DB 5
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRICE APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTONNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-210-172-170
; Sequence 170, Application US/10210172
; Publication No. US20040043928A1
                                                                                                                                                                                                       US-10-161-791-268; Application US/10161791; Sequence 268; Application US/030186863A1; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.3%; Scc...
100.0%; Pre
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INFORMATION FOR SEQ ID NO: 268:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.3
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: peptide US-10-161-791-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 YPPAYP 56
                                                                                  29 KRKKHH 34
                                                                                                                         3 KRKKHH 8
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APPLICANT: Malyankar, Uziel
APPLICANT: Malyankar, Uziel
APPLICANT: Malyankar, Uziel
APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Alsobrook II, John
APPLICANT: Alsobrook II, John
APPLICANT: Lepley, Denise et al.
TILLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
FILE REFERENCE: 21402-416 A 19/210,172
CURRENT APPLICATION NUMBER: 60/329,501
PRIOR APPLICATION NUMBER: 60/329,501
PRIOR APPLICATION NUMBER: 60/319,814
PRIOR APPLICATION NUMBER: 60/310,291
PRIOR APPLICATION NUMBER: 60/310,291
PRIOR APPLICATION NUMBER: 60/310,591
PRIOR APPLICATION NUMBER: 60/310,591
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/310,594
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/310,594
PRIOR APPLICATION NUMBER: 60/311,979
PRIOR APPLICATION NUMBER: 60/311,292
PRIOR APPLICATION NUMBER: 60/311,292
PRIOR APPLICATION NUMBER: 60/311,292
PRIOR APPLICATION NUMBER: 60/311,292
PRIOR APPLICATION NUMBER: 60/313,201
PRIOR FILING DATE: 2001-08-08
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/313,201
PRIOR FILING DATE: 2001-08-13
PRIOR PLING DATE: 2001-08-13
PRIOR PLING DATE: 2001-08-13
PRIOR FILING DATE: 2001-08-13
PRIOR PLING DATE: 2001-08-13
PRIOR PLING DATE: 2001-08-13
PRIOR FILING DATE: 2001-08-13
PRIOR FILING DATE: 2001-08-13
PRIOR FILING DATE: 2001-08-13
PRIOR PRIOR PLING DATE: 2001-08-13
PRIOR PLING DATE: 2001-08-13
PRIOR PRIOR PLING DATE: 2001-08-13
PRIOR PLING DATE: 2001-08-13
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SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 170
LENGTH: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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100.0%; Pred. No. 89;
ive 0; Mismatches
                                                                                   Li, Li
Ji, Weizhen
Padigaru, Muralidhara
Toman, Stacie
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gerlach, Valerie
Hjalt, Tord
Rastelli, Luca
Spytek, Kimberly
Rieger, Daniel
Shimkets, Richard
Zerhusen, Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anderson, David
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Sorman, Linda
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RESULT 15
US-10-424-599-164611
Squarec 164611, Application US/10424599
Fublication No. US20040031072A1
Fublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rowalt David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION UNDRER: US/10/424.599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 164611
LENGTH: 52
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
FEATURE:
NAME/KEX: unsure
LOCATION: (1)...(52)
COTHER INFORMATION: Clone ID: PAT_MRT3847_119661C.1.pep
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0
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10.3%; Score 6; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 0; Indels
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Job time: 47 secs
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35 PYORYP 40
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MOLECULE TYPE: protein
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Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 21, Appli
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 21881, A
Sequence 21881, A
Sequence 20994, A
Sequence 20994, A
Sequence 30311, A
Sequence 30311, A
Sequence 2, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 109, Appli
Sequence 164, Appli
Sequence 164, Appli
Sequence 169, Appli
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164, App
225, App
12246, A
32443, A
6, Appli
9137, Ap
                                                                                           6, 2004, 17:04:44; Search time 18 Seconds (without alignments) 166.350 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
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Sequence 3
Sequence 6
Sequence 9
                                                                                                                                               US-10-079-754A-10
316
1 MKIFIFVFIMALILAMIRAD......QQYQPYQRYPLNYPPAXPFP
                                                                                                                                                                                                                                                                                                                                                                                          Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
    /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
               5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-962-569A-8
US-08-308-883-2
US-08-308-883-2
US-08-256-799-2
US-08-462-437-2
US-09-625-188-20
US-09-625-188-20
US-09-252-991A-27348
US-09-252-991A-27348
US-09-252-991A-27348
US-09-252-991A-27349
US-09-252-991A-27419
US-09-252-991A-20994
US-09-252-991A-20994
US-09-252-991A-20994
US-09-252-991A-20994
US-09-252-991A-20994
US-09-252-991A-20994
US-09-252-991A-30719
US-09-252-991A-30799
                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                            389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
               GenCore version (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum.Match 100%
Listing first 45 summaries
                                                                  - protein search, using sw model
                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length
                           Copyright
                                                                                             August
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
61.5
61
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                                                                    OM protein
                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                              Database
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Sequence 2, Appli
Sequence 2442, A
Sequence 29432, A
Sequence 19832, A
Sequence 10139, A
Sequence 1, Appli
Sequence 17181, A
Sequence 2597, Ap
Sequence 25488, A
Sequence 27610, A
Sequence 29659, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57
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19.9%; Score 63; DB 1; Length 182;
Best Local Similarity 28.8%; Pred. No. 2.3;
Matches 17; Conservative 13; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: MENON, RAVI S.
APPLICANT: GEFERS, KATHLEEN F.
APPLICANT: CHANG, YING-FON
APPLICANT: CHANG, YING-FON
APPLICANT: CHANG, YING-FON
APPLICANT: HAM, RICHARD G.
TITLE OF INVENTION: HUMAN K-CASEIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: FREDERICK W. PEPPER, PH.D.
STREET: 11545 W. BERNARDO COURT, STE. 302
CITY: SAN DIEGO
STATE: CA
COUNTRY: USA
ZIP: 92127
COMPUTER: FREDABLE FORM:
MEDIUM TYPE: FLOPEY disk
COMPUTER: IBM PC COMPATIBLE
OPERATION SYSTEM: PC-DOS/MS-DOS
SUFFACTION NUMBER: US/07/962,569A
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/07/962,569A
ATTORNEY/AGENT INFORMATION:
NAME: PEPPER PH.D. FREDERICK W.
REFERENCE/DOCKET NUMBER: 920224.01
TELEPONDE: (619) 451-1528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: AMINO ACID
TOPOLOGY: Innear
NOTOTION TOPOLOGY: Innear
TYPE: AMINO ACID
TOPOLOGY: Innear
NOTOTION TOPOLOGY: Innear
NOTOTION TOPOLOGY: Innear
TYPE: AMINO ACID
                                                   US-09-252-991A-29449
US-09-252-991A-19832
US-09-252-991A-30139
US-09-865-891A-1
US-09-865-891A-1
US-09-252-991A-18391
US-09-252-991A-27610
US-09-252-991A-27610
US-09-252-991A-27610
US-09-252-991A-27610
US-09-252-991A-29659
US-09-252-991A-29659
US-09-252-991A-29659
US-09-252-991A-29659
US-09-252-991A-29659
US-09-252-991A-29659
US-09-252-991A-32293
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ACCOURT

US-08-730-163-2

US-08-730-163-2

Sequence 2, Application US/08730163

Fatent No. 571250

GENERAL INFORMATION:

APPLICANT: Prieto, P. A.

APPLICANT: Baxter, J. H.

APPLICANT: Cumming, R.D.

TITLE OF INVENTION: Product for Inhibition of Human Rotavirus Infection.

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS: 3

ADDRESSEE: Lonnie R. Drayer

ADDRESSEE: Abbott Laboratories

STREET: 625 Cleveland Avenue

CITY: Columbus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States
COUNTRY: United States
ZIP: 43215
COMPUTER READABLE FORM:
MEDIUM YYER: 3.5 inch, 1.44 Mb storage (B) COMPUTER: Apple Macintosh OPERATING SYSTEM: MacIntosh System 7.1(D) SOFTWARE: ClarisWorks 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/730,163
FILING DATE: US/08/730,163
FILING DATE: 16-SEP-1994
TELECOMMUNICATION NUMBER: US/08/308,882
FILING DATE: US/08/308,882
                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKIFIFVF-IMALILAMIRADSSEEKRHRKRKKHHRGYFQQYQPYQRYPLNY-PPAYPF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MXSFLLVWNALALTLDFLAVEVQNQKQPACHENDERPFYQKTAPY--VPMYYVPNSYPY 57
                                                                                                                                                                                                                                                                                                                                                                       4; Gaps
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 28.8%; Pred. No. 2.3;
Matches 17; Conservative 13; Mismatches 25; Indels
VOLUME:
| ISSUE:
| FSUE:
| PAGES:
| DATE:
| DCCUMENT NUMBER: PCT/W093/15196
| FLING DATE: 25-JAN-1993
| PUBLICATION DATE: 05-AUG-1993
| RELEYANT RESIDUES IN SEQ ID NO: US-08-308-883-2
                                                                                                                              R: PCT/WO93/15196
25-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein.
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DEVELOPMENTAL STAGE:
HARLOOTYPE:
TISSUE TYPE:
CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: Linear
MOLECULE TYPE: Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
ANTI-SENSE:
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CHROMOSONE/SEGMENT:
MAP POSITION:
UNITS:
FRATURE:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
AUTHORS: L. Hansson et al
TITLE: DNA Encoding Kappa-Casein, Process for Obtaining the Protein and Use The
JOURNAL:
                                                               US-08-308-883-2
| Sequence 2, Application US/08308883
| Sequence 2, Application US/08308883
| Sequence 2, Application US/08308883
| Patent No. 5576300
| Patent No. 5576300
| Patent Nukerji, P. APPLICANT: Prieto, P. A. APPLICANT: Baxter, J. H. APPLICANT: Baxter, J. H. APPLICANT: Cummings, M. E.-Y. APPLICANT: Cummings, Res. Patents, J. H. APPLICANT: Cummings, Res. Patents, S. 2 CORRESPONDENCE ADDRESS: 2 CORRESPONDENCE ADDRESS: 3 ADDRESSEE: Lonnie R. Drayer ADDRESSEE: Abort Laboratories STREET: 625 Cleveland Avenue CITY: Columbus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States
ZIP: 43215
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYTEM: Macintosh
OPERATING SYTEM: Macintosh
SOFTWARE: ClarisWorks 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,883
FILING DATE: 16-SEP-1994
CLASSIFICATION: 435
PRICR APPLICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE TRACTERISTICS:
LINEAR AMINO acid
TYPE: Linear
MOLECULE TYPE: Protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
CELL TYPE:
CELL INYE:
CRIL LINE:
ORGANELLE:
INWEDIATE SOURCE:
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FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                      1 MKIFIFVF-IMALILAMIRADSSEEKRHRKRKKKHHRGYFQQYQPYQRYPLNY-PPAYPF 57
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                       4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: HANSON, Lennart

APPLICANT: STROEMOVIST, Mats

APPLICANT: STROEMOVIST, Nats

APPLICANT: BERGSTROEM, Sven

APPLICANT: HENNELL, Olle

APPLICANT: HENNELL, Olle

APPLICANT: FORNALL, Olle

APPLICANT: PORNALL, Olle

APPLICANT: PORNALL, Olle

APPLICANT: FORNELL, Olle

APPLICANT: FORNEL, JUNE PROTEIN, PROCESS

TITLE OF INVENTION: FOR OBTAINING THE PROTEIN AND USE THEREOF

UNDRESSED: ADDRESSES:

ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.9%; Score 63; DB 3; Length 182; 28.8%; Pred. No. 2.3; ative 13; Mismatches 25; Indels
                                                                                                                                                                                                                         Score 63; DB 3; Length 182; Pred. No. 2.3;
                                                                                                                                                                                                                                                                   13; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CUMPOTER: I LEM FC COMPACTION
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,437
FILING DATE: 05-JUN-1995
PRIOR APPLICATION NUMBER: DS #8/92
FILING DATE: 23-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: HANSSON=1A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ...CIEL.
...CESSE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-462-437-2; Sequence 2, Application US/08462437; Patent No. 6232094
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                           Query Match
Best Local Similarity 28.8%;
Matches 17; Conservative 1:
                               TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 182 amino acids
TYPE: amino acid
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Best Local Similarity 28.8<sup>3</sup>
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                       TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-256-799-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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                        TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                   Process for Obtaining the Protein and Use The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 19.9%; Score 63; DB 1; Length 182; Best Local Similarity 28.8%; Pred. No. 2.3; Matches 17; Conservative 13; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT N Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,799
FILING DATE: 06-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: DK 88/92
FILING DATE: 23-JAN-1992
ATTONEY/AGENT INFORMATION:
NAME: APPLICATION: PROPARATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                               LOCATION:
IDENTIFICATION METHOD:
OBENITAR INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: L. Hansson et al
TITLE: DNA Encoding Kappa-Casein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: COOPER, IVET P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: HANSSON=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R: PCT/WO93/15196
25-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOCUMENT NUMBER: PCT/WO93/15190
FILING DATE: 25-JAN-1993
PUBLICATION DATE: 05-AUG-1993
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                        CHROMOSOME/SEGMENT:
MAP POSITION:
    CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C.
COUNTRY: USA
ZIP: 20004
                                                                                                                                                                      UNITS:
FEATURE:
NAME/KEY:
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RESULT 8
US-09-625-188-20
; Sequence 20, Application US/09625188
; Patent No. 6307037
                                                                                                                     , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27856
                                                                                                                                                                                                                                                                                 26 RHRKRKKHHRGYFQQYQP 43
                                                                                                                                                                                                                                                                                                                  40 RHRRRRRHHRGNPQRRRP 57
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                                                                                                                                                                                     Query Match
Best Local Similarity 55.6%;
Matches 10; Conservative
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Best Local Similarity 39.5'
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CRGANISM: Ashbya gossypii
US-09-625-188-20
PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SEQ ID NO 27856
LENGTH: 248
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US-09-134-000C-4463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 20
LENGTH: 729
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ORGANISM:
                                                                                                   TYPE: PRT
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US-05-252-991A-27856
Sequence 27856, Application US/09252991A
PAPEL NO. 6551795
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US 60/074,788
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/094,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKIFIFVF-IMALILAMIRADSSEEKRHRKRKKKHHRGYFQQYQPYQRYPLNY-PPAYPF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MXSFLLVVNALALTLPFLAVEVQNQKQPACHENDERPFYQKTAPY--VPMYYVDNSYPY 57
         1 MKSFLLVVNALALTLPFLAVEVQNQKQPACHENDERPFYQKTAPY--VPMYYVPNSYPY 57
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                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: HANSSON, Lennart
APPLICANT: HANSSON, Lennart
APPLICANT: BERGSTROEM, Sven
APPLICANT: HERNELL, Olle
APPLICANT: HERNELL, Olle
APPLICANT: HERNELL, Olle
APPLICANT: FORENELL, Olle
APPLICANT: FORENELL, Olle
APPLICANT: FORENELL, Olle
APPLICANT: FORENELL, OLL
APPLICANT: TOERNELL, OLL
APPLICANT: CORRESPONDENCE SI
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; · Length 182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTK::

ZIP: 20004
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,437
TILING DATE: 05-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
19.9%; Score 63; DB 3
Best Local Similarity 28.8%; Pred. No. 2.3;
Matches 17; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: CCOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: HANSSON=1A
FELECHWUNICATION INFORMATION:
TELECHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                     Sequence 31, Application US/08462437 Patent No. 6232094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 05-UNA-1995
PRICA APPLICATION DATA:
APPLICATION NUMBER: DK 88/92
FILING DATE: 23-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVer P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 182 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-462-437-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington STATE: D.C.
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## SEQUENCE 4463, Application US/09134000C

| Sequence 4463, Application US/09134000C
| Patent No. 6617156
| GENERAL INFORMATION:
| APPRILGATY Lyan Doucette-Stamm et al Anno ACID SEQUENCES RELATING TO TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTERCECCE: 032796-032
| CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT PILING DATE: 1998-08-13
| PRIOR PAPICATION NUMBER: US 60/055,778
| PRIOR PAPICATION NUMBER: US 60/055,778
| NUMBER OF SEQ ID NOS: 6812
| SEQ ID NO 4463
| LENGTH = 620
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                                             Gaps
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Length 248;
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                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 LLLKSIK----KSLRHRRRIPMQTKKIHFGAFSRFKPYLLRYP 54
                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: No. 637037artis AG
TITLE OF INVENTION: Fungal Target Genes and Methods
FILE REFERENCE: PB/5-31285P1
CURRENT APPLICATION WUMBER: US/09/625,188
CURRENT FLING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 494 SQSSQAHSQQHQQQHQQQQQQQQQQQQQQQQQPPQQP 530
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Pred. No. 15;
7; Mismatches
  4 ;
                      Pred. No. 4.2;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
19.5%; Score 61.5; D
Best Local Similarity 32.4%; Pred. No. 16;
Matches 12; Conservative 9; Mismatches
B
Score 62;
Pred. No.
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Sequence 20994, Application US/09252991A
Sequence 20994, Application US/09252991A
Sequence 20994, Application US/09252991A
Sequence 20994, Application US/09252991A
APPLICANT: Marc U. Rubenfield et al.
APPLICANT: Marc U. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REPRENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR PLILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
SEQ ID NO 20994
SEQ ID NO 20994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: MATC J. Rubenfield et al.

APPLICANT: MATC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEUC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27419
                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 247;
                                                                                                                                                                                                                                                                                                                Length 720;
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18.5%; Score 58.5; DB 4;
Best Local Similarity 39.4%; Pred. No. 11;
Matches 13; Conservative 6; Mismatches 11;
                                                                                                                                                                                                                                                                                                           Score 59; DB 4;
Pred. No. 32;
B; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 RADSSEEKRHRKRKKHHRGYFQQYQPYQRYPLN
CURRENT FILING DATE: 1999-02-18
PRIOR PEDICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21881
LENGTH: 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-252-991A-27419
; Sequence 27419, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 29.8%;
Matches 14; Conservative
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US-09-252-991A-20994
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CRGANISM: Pseudo
US-09-252-991A-20994
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                                                                                                                                                                                                               TYPE: PRT
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                                                               Sequence 16948, Application US/09252991A
Sequence 16948, Application US/09252991A
Sequence No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION:
APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16848
LENGTH: 271
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APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDCMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US/06/094,190
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27348
LENGTH: 225
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Patent No. 6551795
General INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 59, DB 4; Length 225;
Pred. No. 8.9;
7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQAGEQVRQRRKKEDAADQGEARQTVEPPQFHPLAIDPAYP 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27348, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 33.3%;
Matches 18; Conservative
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Best Local Similarity 39.0%
Matches 16; Conservative
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RESULT 15

US-09-252-91A-30311

Sequence 30311, Application US/09252991A

Patent No. 6521795

GENERAL INFORMATION:

APPLICATION:

APPLICATION:

TITLE OF INVENTION:

PILE REPERENCE:

TITLE OF INVENTION:

PILOR APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,786

PRIOR APPLICATION NUMBER: US 60/074,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 30311

LENGTH'S 521
                                                         ä
                                                         Gaps
Query Match
18.5%; Score 58.5; DB 4; Length 333;
Best Local Similarity 38.7%; Pred. No. 16;
Matches 12; Conservative 5; Mismatches 11; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 36.7%; Pred. No. 30;
Matches 18; Conservative 6; Mismatches 21; Indels
                                                                                                                                      25 KRHRKRK---KHHRGYFQQYQPYQRYPLNYP 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Pseudomonas aeruginosa
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Gaps

12 LILAMIRADSSE--EKRHRKRKKHHRGYFQQYQPYQRYPLNYPPAYPFP 58

Search completed: August 6, 2004, 17:05:15 Job time: 19 secs

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August 6, 2004, 17:04:44; Search time 47 Seconds (without alignments) 387.098 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/PUT_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/PUT_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*
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| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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316
1 MKIFIFVFIMALILAMIRAD......QQYQPYQRYPLNYPPAXPFP
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 7, Appli Sequence 10, Appli Sequence 12, Appli Sequence 11, Appli Sequence 11, Appli Sequence 168, App Sequence 6, Appli Description 3 US-10-079-754A-7 3 US-10-079-754A-10 3 US-10-079-754A-8 3 US-10-079-754A-11 3 US-10-079-754A-11 3 US-10-079-754A-11 5 US-10-210-17-168 US-09-917-340-19 US-09-992-035B-6 US-09-992-035B-6 US-09-992-035B-6 US-09-999-570-6 US-09-999-570-6 US-09-999-6-6 US-10-000-889-6 US-10-154-678-6 DB Query Match Length Result

Sequence 192104,	equence 19	2041,	equence 7176	209	⋖.	e 19198	210	e 1919	equence 188109	equence 1457,	equence 19213	Sequence 192071,	equence 19209	equence 1			equence 1922	equence 17953	Н	e 1919	Sequence 192057,	Sequence 192167,	equence 19209	equence 1921	e 17954	e 19217	e 19210	e 19216	Sequence 192165,
US-10-43	US-10-437-963-19217	US-10-437-963-19204	US-10-282-122A-7	US-10-437-963-19209	US-10-631-581-	US-10-437-963-19198	US-10-437-963-1	US-10-437-963-19198	US-10-437-963-1881	US-10-374-780A-145	US-10-437-963-192	US-10-437-963-19207;	US-10-437-963-192	US-10-374-780A-145	US-10-374-780A-145	US-10-437-963-1921	US-10-437-963-19221	US-10-437-963-17953	US-10-437-963-19205	US-10-437-963-19199	US-10-437-963-192	US-10-437-963-19	US-10-437-963-1920	US-10-437-963-19	US-10-437-963-1795	US-10-437-963-19	US-10-437-963-19210	US-10-437-963-1921	US-10-437-963-192165
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ALIGNMENTS

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                                    US-10-10/3-5944.

Sequence 7, Application US/10079754A.

Publication No. US20020164625A1

SEMBRAL INPORMATION:

APPLICANT: Glenn, Marthew

APPLICANT: Glenn, Marthew

APPLICANT: Glenn, Marthew

APPLICANT: Glenn, Marthew

APPLICANT: Davis, Stephen R.

TITLE OF INVENTION: Compositions Isolated from Bovine

TITLE OF INVENTION: Marmary Gland and Methods for Their Use

FILE REFERENCE: 11000.1068

CURRENT APPLICATION NUMBER: US/10/79, 754A

CURRENT APPLICATION NUMBER: US 09/699, 146

PRIOR APPLICATION NUMBER: US 09/699, 146

PRIOR PILING DATE: 2000-10-27

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 1999-00-32

PRIOR FILING DATE: 1999-00-32

PRIOR FILING DATE: 1999-08-23

WUMBER OF SEQ ID NOS: 15

SEQ ID NOS: 15

SEG ID NO 7

TEMBRE OF SECURE WINDOW WINDOW. US NUMBER: US NO 150, 330
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100.0%; Score 316; DB 13; Length 58;
Best Local Similarity 100.0%; Pred. No. 5.6e-30;
Matches 58; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CRGANISM: Bovine
US-10-079-754A-7
RESULT 1
US-10-079-754A-7
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APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Mammary Gland and Methods for Their Use
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
FILE REPERBACE: 11000.1068
CURRENT APPLICATION NUMBER: US/10/079,754A
CURRENT FILING DATE: 2002-02-19
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-08-22
PRIOR PILING DATE: 2000-08-22
PRIOR PLING DATE: 2000-08-22
PRIOR PILING DATE: 12000-08-22
PRIOR PILING DATE: 12000-08-22
PRIOR PILING DATE: 12000-08-23
PRIOR PILING DATE: 1200-08-23
PRIOR PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Grigor, Marray R.
APPLICANT: Grigor, Marray R.
APPLICANT: Davis, Stephen R.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
FILE REFERENCE: 11000.1068
CURRENT APPLICATION NUMBER: US/10/079,754A
CURRENT PILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1000-10-27
PRIOR FILING DATE: 1000-10-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKIFIFVFIMALILAMIRADSSEEKRHRKRKKHH 34
                                                                                                                                                                                                                                                                                   Sequence 12, Application US/10079754A Publication No. US20020164625A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-079-754A-12
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GENERAL INFORMATION:
APPLICANT: Glein, Matthew
APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
ITILE OF INVENTION: Mammary Gland and Methods for Their Use
FILE REFERENCE: 11000.1068
CURRENT APPLICATION NUMBER: US/10/079,754A
CURRENT APPLICATION NUMBER: US 09/699,146
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SOFWWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 58
                                                                JULY SEQUENCE 10, Application US/10079754A

| Sequence 10, Application US/10079754A
| Publication No. US20020164625A1
| GENERAL INPORMATION:
| APPLICANT: Grigor, Murray R.
| TITLE OF INVENTION: Compositions Isolated from Bovine
| TITLE OF INVENTION: Compositions Isolated for Their Use
| TITLE OF INVENTION: Mammary Gland and Methods for Their Use
| TITLE OF INVENTION: Mammary Gland and Methods for Their Use
| FILE REFERENCE: 11000.1068
| CURRENT APPLICATION NUMBER: US/09/699,146
| PRIOR FILING DATE: 2000-10-27
| PRIOR PELLING DATE: 2000-10-27
| PRIOR PELLING DATE: 2000-06-22
| PRIOR APPLICATION NUMBER: US 69,162,701
| PRIOR FILING DATE: 1999-108-23
| NUMBER OF SEQ ID NOS: 15
| SEQ ID NO 10
| SEQ ID NO 10
| LENGTH SET
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Best Local Similarity 100.0%; Pred. No. 5.6e-30;
Matches 58; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Bovine US-10-079-754A-10
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CRGANISM: Bovine
US-10-079-754A-8
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RESULT 3

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APPLICANT: MacDugall, John
APPLICANT: Alsobrook II, John
APPLICANT: Alsobrook II, John
APPLICANT: Alsobrook II, John
APPLICANT: Lepley, Denise et al.
TITLE REPRENCE: 2100-416
TITLE REPRENCE: 2100-416
TITLE REPRENCE: 2100-60-02
FILE REPRENCE: 2100-60-02
FILE REPRENCE: 2100-60-02
FILE REPRENCE: 2001-60-02
FILE REPRENCE: 2001-60-02
FILE CATION NUMBER: 60/309,501
FILE REPRENCE: 2001-60-02
FILE REPRENCE: 2001-60-02
FILE REPRENCE: 2001-60-02
FILE REPRENCE: 2001-60-03
FILE REPRENCE: 2001-
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; Sequence 19, Application US/09917340
; Patent No. US2002009369A1
; GENERAL INFORMATION:
    APPLICANT: MUTPLY, Christopher J.
    APPLICANT: MCADNILY, Jonathan F.
    APPLICANT: McADNILY, Jonathan F.
    APPLICANT: Reid, Ted W.
    TITLE OF INVENTION: Transplant Media
    FILE REFERENCE: TPLANT-06468
    CURRENT APPLICATION NUMBER: US/09/917,340
    CURRENT FILING DATE: 2000-07-28
    PRIOR FILING DATE: 2000-07-28
    PRIOR FILING DATE: 2000-07-28
    PRIOR FILING DATE: 2000-01-28
    PRIOR APPLICATION NUMBER: 60/249,602
    PRIOR APPLICATION NUMBER: 60/290,932
    PRIOR FILING DATE: 2000-105-15
    NUMBER OF SEQ ID NOS: 96
              Gerlach, Valerie
Hjalt, Tord
Rastelli, Luca
Spytek, Kimberly
                                                                                                                                                                                                                                  Malyankar, Uriel
MacDougall, John
                                                                                                                                                            Edinger, Shlomit
Ellerman, Karen
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ORGANISM: Homo sapiens
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APPLICANT:
APPLICANT:
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Sequence 11, Application US/10079754A
FUBLICARLION No. US20020164625A1
GENERAL INFORMATION:
APPLICANT: Glenn, Matthaw
APPLICANT: Glenn, Matthaw
APPLICANT: Glenn, Matthaw
APPLICANT: Glenn, Matthaw
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: OWNER: US 0100/10/69
FURRENT PAPLICATION NUMBER: US 09/699,146
FRICA PAPLICATION NUMBER: US 09/699,146
FRICA FILING DATE: 1999-10-29
FRICA FILING DATE: 1999-10-29
FRICA FILING DATE: 1999-10-29
FRICA FILING DATE: 2000-10-27
FRICA FILING DATE: 1999-10-29
FRICA FILING DATE: 1999-10-29
FRICA FILING DATE: 1999-10-29
FRICA FILING DATE: 1000-08-22
FRICA REPLICATION NUMBER: US 60,150,330
FRICA FILING DATE: 1000-08-22
FRICA FILING DATE: 1000-08-23
FRICA FILING DATE: 1000-08-23
FRICA FILING DATE: 1000-08-23
FRICA FILING DATE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
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                                                           53.5%; Score 169; DB 13; Length 70; 97.1%; Pred. No. 1.7e-12; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                        1 MKIFIFVFIMALILAMIRADSSEEKRHRKRKKHH 34
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APPLICANT: Miller, Charles; APPLICANT: Parturajan, Meera APPLICANT: Rieger, Daniel APPLICANT: Rieger, Daniel APPLICANT: Sinkets, Richard APPLICANT: Srinkets, Richard APPLICANT: Zerhusen, Bryan APPLICANT: Li, Li, Li, APPLICANT: Li, Li, Li, APPLICANT: Casman, Stacie APPLICANT: Casman, Stacie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 FOOYOPYORYPLNYPPAYP 56
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                                     Query Match
Best Local Similarity 97.19
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Gorman, Linda
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Guo, Xiaojia
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Best Local Similarity
Matches 18; Conserv
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US-10-079-754A-9
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; Sequence 6, Application US/09999570; Publication No. US20030170628A1; GENERAL INFORMATION:
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Matches 18; Conservative
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Best Local Similarity 32.7%
Matches 18; Conservative
                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                            ; NAME/KEY: SIGNAL
; LOCATION: 1..19
US-09-924-340-6
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; LOCATION: 1..19
US-09-992-095B-6
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SOFTWARE: JPat
SEQ ID NO 6
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US-09-999-570-6
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JOSEQUENCE 6, Application US/09992600A

Publication No. US20030027161A1

GENERAL INFORMATION:

APPLICANT: Tennian, Stephane

APPLICANT: Tennian, Stephane

APPLICANT: Tennian, HUMAN CDNAS AND PROTEINS AND USES THEREOF

FILE REFERENCE: 91.US4.D1V

CURRENT APPLICATION HUMBER: US/09/992,600A

CURRENT FILING DATE: 2001-11-13

PRIOR FILING DATE: 2001-08-06

PRIOR FILING DATE: 2001-08-06

PRIOR PLICATION NUMBER: US 60/305,456

PRIOR PLICATION NUMBER: US 60/305,456

PRIOR PLICATION NUMBER: US 60/305,456

PRIOR FILING DATE: 2001-08-06

PRIOR FILING DATE: 2001-06-15

PRIOR PLICATION NUMBER: US 60/302,277

PRIOR PLICATION NUMBER: US 60/298,698

PRIOR FILING DATE: 2001-06-25

PRIOR PLING DATE: 2001-06-25

PRIOR PLING DATE: 2001-06-25

NUMBER OF SEQ ID NOS: 114

SEQ ID NO 6

LINGTH: 78
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Publication No. US20030027248A1
GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUVAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US2.RER: US/09/924,340
CURRENT APPLICATION NUMBER: US/09/924,340
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR PLICATION NUMBER: US 60/302,277
                                                                                                                                                                                                                                                                                         1 MKFFVFALILALMLSMTGADSHAKRHHGYKRKFHEKHHSHRGYRSNY 47
                                                                                                                                                                                                                                                             1 MKIFIFVFIMALILAMIRADSSEEKRH-RKRKKH-----HRGYFQQY 41
                                                                                                                                                                 DB 9; Length 51;
                                                                                                                                                                                                            13; Indels
                                                                                                                                                                 Query Match
30.1%; Score 95; DB 9; I
Best Local Similarity 46.8%; Pred. No. 0.00067;
Matches 22; Conservative 6; Mismatches 13;
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                   TYPE: PRT
CRGANISM: Homo sapiens
US-09-917-340-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 18; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..19
US-09-992-600A-6
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US-09-924-340-6
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PRICE FILING DATE: 2001-06-15

PRICE PLOY FILING DATE: 2001-06-15

PRICE PLOY FOR THING DATE: 2001-06-15

PRICE PLOY FOR THING DATE: 2001-06-15

PRICE PLOY FOR THING DATE: 2001-06-25

PRICE PLOY FOR THING DATE: 2001-06-26

PRICE PLOY FOR THING DATE: 20
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Query Match
29.9%; Score 94.5; DB 14; Length 78;
Best Local Similarity 32.7%; Pred. No. 0.0012;
Matches 18; Conservative 13; Mismatches 17; Indels
                                     17; Indels
                                                                                                                                                                      1 MKFFVFALVLALMISMISADSHEKRHGYRRFH---
Best Local Similarity 32.7%; Fred. No. 0.0012;
Matches 18; Conservative 13; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/10000986 Publication No. US20030096247A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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; NAME/KEY: SIGNAL
; LOCATION: 1..19
US-10-000-986-6
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Sequence 6. Application US/10000489

Publication No. US203092011A1

GENERAL INFORMATION:

APPLICANT: Benjamin, Stephane

APPLICANT: Benjamin, Stephane

APPLICANT: Tanaka, HIYCOAKI

TILE OF INVENTUON: HUMAN CDNAS AND PROTEINS AND USES THEREOF

FILE REFERENCE: 91.US6.D1V.

CURRENT APPLICATION NUMBER: US/10/000,489

CURRENT APPLICATION NUMBER: US 09/924,340

PRIOR FILING DATE: 2001-08-06

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-25

NUMBER OF SEQ ID NOS: 112

SOFTWARE: JEAUCHT
                        APPLICANT: Designation, occupants, APPLICANT: Tanaka, Histoaki, TILLE OF INVENTION: HUMAN CDNAS AND PRCTEINS AND USES THEREOF FILE REFERENCE: G-0910508DIV
CURRENT APPLICATION NUMBER: US (09/99,570
CURRENT APPLICATION NUMBER: US (09/924,340
PRIOR PLICATION NUMBER: DC 01-06-06
PRIOR FILING DATE: 2001-08-06
PRIOR PRILING DATE: 2001-08-06
PRIOR PRILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR PRILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-15
PRIOR PRILING DATE: 2001-06-15
PRIOR PRILING DATE: 2001-06-15
PRIOR PRILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-15
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29.9%; Score 94.5; DB 10; Length 78;
Best Local Similarity 32.7%; Pred. No. 0.0012;
Matches 18; Conservative 13; Mismatches 17; Indels
        APPLICANT: Benjanin, Stephane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..19
US-10-000-489-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: SIGNAL
; LOCATION: 1..19
US-09-999-570-6
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1 MKIFIFVFIMALILAMIRADSSEEKRHRKRKKKHHRGYFQQYQPYQRYPLNYPPAY 55
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                                                                                                  --EKHHSYHITLLPLF 48
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| Sequence 6, Application US/10154678
| Publication No. US2030162186A1
| GENERAL INFORMATION:
| APPLICANT: Benjanin, Stephane
| APPLICANT: Tanaka, Hiroaki
| TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
| FILE REFERENCE: 182.USI.REG
| CURRENT FILING DATE: 2002-10-15
| PRIOR FILING DATE: 2001-0-15
| PRIOR PLILING DATE: 2001-0-7-13
| PRIOR PLILING DATE: 2001-0-7-15
| PRIOR PLILING DATE: 2001-05-25
| WUMBER OF SEQ ID NOS: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INCOMANTION:
GENERAL INCOMANTION:
APPLICANT: Tanaka, Hiroaki
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US9.DIV
CURRENT APPLICATION NUMBER: US/10/000,986
CURRENT APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 14;
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7;

Search completed: August 6, 2004, 17:09:58 Job time : 51 secs

Sequence 17, Appl Sequence 7, Appli Sequence 1, Appli Sequence 1, Appli Patent No. 5198347 Sequence 3, Appli Sequence 3, Appli

Sequence 1, Sequence 1,

Sequence 30, Sequence 28, Sequence 28, Sequence 28, Sequence 28, Sequence 28, Sequence 28, Sequence 17, Sequence 17, Sequence 17,

Sequence 71, Sequence 71, Sequence 33, Sequence 33, Sequence 34, Sequence 33, Sequence 34,

Sequence 38,

Sequence 38,

Sequence

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Sequence 56, Application US/08434099A

Parent No. 6083902

GENEAL INFORMATION:

TITLE OF INVENTION: Recombinant Fibrin Chains,

TITLE OF INVENTION: Fibrin and Fibrin-Homologs

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSES E. R. Squibb & Sons, Inc.

STREET: 100 Headquarters Park Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: DEM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastESC for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/434,099A FILING DATE: 03-MAY-1995 CLASSIFICATION NUMBER: US/08/236,979 FILING DATE: 02-MAY-1994 ATTORNEY/AGENT INFORMATION: NAME: FURMEN, US 08/236,979 FILING DATE: US-MAY-1994 ATTORNEY/AGENT INFORMATION: NAME: FURMEN, US 08/236,979 REGISTRATION NUMBER: 30,942 REFERENCE/DOCKET NUMBER: CV0054a TELLECOMPUNICATION INFORMATION: TELLEPHONE: 900-281-2372
US-08-486-663A-17

US-08-47-904B-7

US-08-435-637A-1

US-08-435-637A-1

US-08-435-637A-1

US-08-434-38-1

US-08-632-580A-3

US-08-632-580A-3

US-08-632-580A-3

US-08-632-580A-3

US-08-955-171E-37

US-08-956-171E-37

US-08-956-171E-37

US-08-956-171E-37

US-08-956-171E-37

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US-08-96-171E-37

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US-08-441-153-28

US-08-441-153-28

US-08-441-153-28

US-08-481-710-33

US-08-481-710-33
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TELEX:
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CITY: Ski
STATE: NC
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-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOF=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26, Appli
Sequence 5, Appli
Sequence 1550, Ap
Sequence 1164, Ap
Sequence 2340, Ap
Sequence 2770, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 28, Appli
                                                                                                                          August 16, 2004, 00:50:06; Search time 61 Seconds (without alignments) 527.658 Million cell updates/sec
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                                                                                                                                                                                                                               1 MKIFIFVFIMALILAMIRAD......QQYQPYQRYPLNYPPAYPFP 58
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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                          nucleic search, using frame_plus_p2n model
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US-08-206-176-5
US-09-543-681A-1164
US-09-134-000C-1868
US-09-134-000C-1868
US-09-543-681A-2340
US-09-543-681A-2670
US-09-543-681A-2670
US-08-237-401A-3
US-08-08-09-4
US-08-08-09-4
US-08-074-030-4
US-08-674-030-4
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                                                                                                                                                                                                                                                                                 5 60.0 , Xgapext 60.0
5 60.0 , Ygapext 60.0
6.0 , Fgapext 7.0
6.0 , Delext 7.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued Patents NA:*
                                                                                                                                                                                        US-10-079-754A-10
58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length DB
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10564
11062
11509
12082
2437
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2619
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Ygapop 6
Fgapop
Delop
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                                                                                                                                                                                                Title:
Perfect score:
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us-10-079-754a-10.rni

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.05-08-206-176-5
; Sequence 5, Application US/08206176
; Patent No. 5639940
; GENERAL INFORMATION:
APPLICANT: Dalrymple, Michael A
APPLICANT: Proster, Donald C
TITLE OF INVENTION: Production of Fibrinogen in Transgenic
TITLE OF INVENTION: Animals
TITLE OF INVENTION: Animals
TITLE OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: Seattle
CITY: Seattle
CITY: Seattle
COUNTRY: USA
ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: join(1799..1876, 1973..2017, 2207..2390, 2510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NATE: US/08/206,176
FILING DATE:
                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                            US-10-079-754A-10 (1-58) x US-08-434-099A-26 (1-1438)
                                                                                                                                                                                                                                                                                                                              Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: human fibrinogen gamma chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: PATKER, GATY B
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-15
TELECOMMUNICATION INFORMATION:
TELEPRONE: 206-544-8080 ext 322
TELEPRONE: 206-548-2329
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 MetAlaLeuIleLeuAlaMetIle 17
INFORMATION FOR SEQ ID NO: 26
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                              NAME/KEY: Coding Sequence;

LOCATION: 3...1364

OTHER INFORMATION:

US-08-434-095A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 10564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                           100.00%
                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                   Alignment Scores:
Pred. No.:
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MS-09-543-681A-1164

Sequence 1164, Application US/09543681A

Sequence 1164, Application US/09543681A

Sequence 1164, Application US/09543681A

Sequence 1164, Application US/09543681A

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000.04-05

FRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 1164

LENGTH: 1062
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US-09-543-681A-2950
US-09-543-681A-2950
Sequence 2950, Application US/09543681A
Sequence 2950, Application US/09543681A
Sequence 2950, Application US/09543681A
Sequence 2950, Application US/09543681A
THEOREMEAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL)
TITLE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: UNMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT PILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 2950
LENGTH: 711
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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7.00
100.00%
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12.07%
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13.79%
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; ORGANISM: Proteus mirabilis
US-09-543-681A-1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
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    , LOCATION:
, LOCATION:
US-08-206-176-5
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Pred. No.:
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Alignment Scores:

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US-09-543-681A-2670/C
US-09-543-681A-2670/C
Batent No. 6605709
Batent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL1
TITLE OF INVENTION: UNMER: US/09/543,681A
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION WUMBER: US/09/543,681A
CURRENT FILING DATE: 1099-04-09
PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-456-647B-3/C

Sequence 3, Application US/08456647B

Patent No. 581816

GENERAL INFORMATION:

APPLICANT: Lemke Ph.D. et al., Greg E.

TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES

NUMBER OF SEQUENCES: 54

CORRESPONDENCES: 54

CORRESPONDENCE FISH & RICHARDSON P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,647B
FILING DATE: 02-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-079-754A-10 (1-58) x US-09-543-681A-2670 (1-2082)
                                                                                                US-10-079-754A-10 (1-58) x US-09-543-681A-2340 (1-1914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [ndels:
                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/237,401
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1399 TACCCGCCAGCGTATCCATT 1379
                                                                                                                                                                                                   669 ATCTTCATCTTCGTCTTCATC 649
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                                                                                                                                                           3 IlephellePhevalPhelle 9
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100.00%
12.07%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA; ORGANISM: Proteus mirabilis US-09-543-681A-2670
      12.07%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 2670
LENGTH: 2082
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Best Local Similarity:
Query Match:
DB:
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      Query Match:
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Sequence 2340, Application US/09543681A

Sequence 2340, Application US/09543681A

Sequence 2340, Application US/09543681A

Patent No. 6605709

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| Sequence 1868, Application US/09134000C
| Sequence 1868, Application US/09134000C
| Patent No. 6617156
| GENERAL INFORMATION:
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
| TITLE OF INVENTION: ENTERCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS
| FILE REFERENCE: 032796-032
| CURRENT APPLICATION NUMBER: US/09/134,000C
| CURRENT FILING DATE: 1998-08-13
| PRIOR APPLICATION NUMBER: US 60/055,778
| PRIOR APPLICATION NUMBER: US 60/055,778
| NUMBER OF SEQ ID NOS: 6812
| SEQ ID NO 1868
| SEQ ID NO 1868
| LENGTH: 1509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-079-754A-10 (1-58) x US-09-134-000C-1868 (1-1509)
                                                                                                                                                                                                                              US-10-079-754A-10 (1-58) x US-09-543-681A-1164 (1-1062)
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154
7.00
100.00%
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100.00%
12.07%
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12.07%
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; ORGANISM: Proteus mirabilis
US-09-543-681A-2340
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SEQ ID NO 2340
LENGTH: 1914
                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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Pred. No.:
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Pred. No.:
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      Pred. No.:
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STRANDEDNESS: single

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Sequence 3, Application US/08237401A

Sequence 1, Application US/08237401A

GENERAL INFORMATION:
APPLICANT: Lender Ph.D. et al., Greg E.
TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALP: 9203,
CALP: 9203,
CALP: 9203,
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,401A
FILING DATE: 02-MAY-1994
CLASSIFICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
CILASSIFICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Haile Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07251/007001
TELEPHONE: (619) 678-5070
TELEPHONE: (619) 678-5070
TELEPAX: (619) 678-5070
TELEPAX: (619) 678-5070
TELEPAX: (619) 678-5070
SEQUENCE CHARACTERISTICS:
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Matches:
Conservative:
Mismatches:
Indels:
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ATTORNEY/AGENT INFORMATION:

NAME: Wetherell Ph.D., John R.
REGISTRATION NUMBER: 31.678
REPERENCE/DOCKET NUMBER: 07251/007002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO. 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2437 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      565 ATACTTGCCATGATCAGAGCC 545
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                  ) NAME/KEY:
; LOCATION:
US-08-456-647B-3
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DB:
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Sequence 4, Application US/08100692
| Sequence 4, Application US/08100692
| Patent No. 5532348
| GENERAL INFORMATION:
| APPLICANT: Hubbregese, Jon M. APPLICANT: Scheffner, Martin APPLICANT: Scheffner, Martin APPLICANT: Howley, Peter M. TITLE OF INVENTION: TEREOF TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF TOWNERS OF SEQUENCES: 6 CORRESPONDENCE ADDRESS: ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Street Tower CITY: San Francisco CITY: San Francisco CITY: CAN STATES CAN STATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SITALE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Flappy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION NUMBER: US/08/100,692
FILING DATE: 19930730
CLASSIFICATION NUMBER: 31,990
REPRENCEY/AGENT INFORMATION:
NAME: PARTHELE-SLEVEN W.
REGISCOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHRAPATERISTICS:
LENGTH: 2598 base pairs
                                                                                                                                                                                                                                                                                                     Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid STRANDEDNESS: sing
STRANDEL
TOPOLOGY: 111...
MOLECULE TYPE: DNA
IMMEDIATE SOURCE:
CLONE: TYRO-2
; FRATURE:
; NAME/FRY: CDS
;
LOCATION: 3...
US-08-237-401A-3
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Best Local Similarity:
Query Match:
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Pred. No.:
Score:
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US-08-100-692-4/c
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, LOCATION:
US-08-100-692-4
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APPLICANT: State the state of t
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ZIP: 94105-1492
ZIP: 94105-1492
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OMPUTER: IBM FC compatible
OMPUT
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Matches:
Conservative:
Mismatches:
Indels:
                   Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08674030 Patent No. 5914389 GENERAL INFORMATION:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 1010..1321
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Best Local Similarity:
Query Match:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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543 ATCTTCATCTTTGTCTTCATC 523

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APPLICANT: Scandar, Matthew
APPLICANT: Chen, Yao
APPLICANT: Chen, Yao
APPLICANT: Chen, Yao
APPLICANT: Stockert, Elisabeth
APPLICANT: Old, Lloyd
APPLICANT: Old, Lloyd
APPLICANT: Muth, Alex
APPLICANT: Muth, Alex
APPLICANT: Muth, Alex
APPLICANT: Muth, Alex
TITLE OF INVENTION: Renal Cancer Associated Antigens and
TITLE OF INVENTION: Uses Therefor
TITLE OF THE REPERSOR INVENTION UNMER: US 09/166,350
EARLIER PILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 28
ILENGTH: 2619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-08-486-663A-17/C
i Sequence 17, Application US/08486663A
i Patent No. 5968761
i GENERAL INFORMATION:
APPLICANT: Rolle, Mark
i APPLICANT: Draetta, Giulio
APPLICANT: Guiliaume Cottarel
TITLE OF INVENTION: Ubiquitin Conjugating Enzymes
NUMBER OF SEQUENCES: 21
CORRESPONDENCE LAHIVE & COCKPIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-079-754A-10 (1-58) x US-09-166-350-28 (1-2619)
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,663A
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
              Sequence 28, Application US/09166350A Patent No. 6440663 GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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100.00%
12.07%
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CRGANISM: Homo sapiens
US-09-166-350-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
STATE: MA
COUNTRY: USA
US-09-166-350-28/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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US-10-079-754A-10 (1-58) x US-08-767-942A-20 (1-2624)
, LOCATION: 1..2624
US-08-247-904B-7
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Patent No. 5981699
GENERAL INFORMATION:
APPLICANT: Roife, Mark
APPLICANT: Desetta, Giulio
TITLE OF INVENTION: Human Ubiquitin Conjugating Enzyme
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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STATE: MA
COMPUTER READABLE FORM:
MEDLIUM TYBE: R-DEDBY disk
COMPUTER: 120 PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/247,904B
FILING DATE: 23 -MAY-1994
CLASSIFICATION STORMS: NOMBER: MSCIICATION: TELECOMMUTICATION INFORMATION:
REGISTRATION NUMBER: MSCINGS
REFERENCE/DOCKET NUMBER: MIV-029.01
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION INFO
   REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-029CP2
TELECOMMUNICATION:
TELEFONE: (617) 227-7400
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2624 base pairs
TYPE: nucleic acid
TYPE: TYPE: CDNA
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STRANDEDNESS: both
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Best Local Similarity:
Query Match:
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; LOCATION: 1...2
US-08-486-663A-17
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CITY: Boston
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Sequence 0. Application US/08767942A
Patent No. 6068982
GENERAL INFORMATION:
APPLICANT: Rolfe, Mark
APPLICANT: Chiu, M. Isabel
APPLICANT: Damagnez, Veronique
APPLICANT: Damagnez, Veronique
APPLICANT: Damagnez, Veronique
APPLICANT: Guillaume, Cottarel
TITLE OF INVENTION: UBIQUITIN CONJUGATING ENZYMES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPENDENCE ADDRESS:
CORRESPONDENCE AD
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CITY: Boston
CITY: Boston
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: US/OB/767,942A
FILING DATE: 17-DEC-1996
ATTORNEY AGENT INPORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: MY-029.04
RETERENCE/DOCKET NUMBER: MY-029.04
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TEMPERATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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TYPE: nucleic acid
STRANDEDNESS: both
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MOLECULE TYPE: CDNA
FEATURE:
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Best Local Similarity:
Query Match:
                                                                               Score:
Percent Similarity:
Best Local Similarity:
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; LOCATION: 1..2
US-08-767-942A-20
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US-08-767-942A-20/c
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Pred. No.:
Alignment Scores:
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DB:
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* Tue Aug 17 16:21:37 2004

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Search completed: August 16, 2004, 01:14:03 Job time : 68 secs

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Sequence 1, Appliance 2, Appliance 4, Appliance 4, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 13, Appliance 1815, Appliance 1825, Appliance 1821, Appliance 1832, Appliance 1832, Appliance 1832, Appliance 1832, Appliance 1832, Appliance 1833, Appliance 1834, Appliance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 148, App
Sequence 36128, A
Sequence 60602, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence (Sequence (
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Sequence 15, Application US/10079754A

Publication No. US20020164625A1

GENERAL INFORMATION:

APPLICANT: Glenn, Matthew

APPLICANT: Grigor, Murray R.

APPLICANT: Grigor, Murray R.

APPLICANT: Molenar, Adrian J.

APPLICANT: Molenar, Adrian J.

TITLE OF INVENTION: Compositions Isolated from Bovine

TITLE OF INVENTION: Compositions Isolated from Govine

TITLE OF INVENTION: Domes: 1100.1068

CURRENT APPLICATION NUMBER: US/10/079,754A

CURRENT FILING DATE: 2002-02-19

FRIOR FILING DATE: 2000-10-27

PRIOR APPLICATION NUMBER: US 60,162,701

PRIOR FILING DATE: 1999-10-29

PRIOR APPLICATION NUMBER: US 60,162,701

PRIOR PELING DATE: 2000-08-22

PRIOR PELING DATE: 1999-10-29

PRIOR PILING DATE: 1000-08-23

PRIOR FILING DATE: 1000-08-23

NUMBER OF SEQ ID NOS: 15
ALIGNMENTS
       267
505
505
505
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525
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1726
1339
339
464
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/CGM2 1/USPTQ_spool/US10079754/runat_06082004_181357_2954/app_query.fasta_1.199
-Q=/CGM2 1/USPTQ_spool/US10079754/runat_06082004_181357_29554/app_query.fasta_1.199
-DB=Published_Applications_NA -QFMT=fastap -SUPFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -ENN=-1 -MATRIX=01150
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -TRR SCORE=quality -THR_MN=1
-ALIGN=15 -MODE=LOCAL -OUTPWT=pto -NORM=ext -HEAPSTZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10079754 @CGN 1 1.480 @runat_06082004 181357_29954
-NCPIG= -INCPUE3 -NO MAAP -LARGEQUERY -NGG $CORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOTT=120 -WARN TIMEOTT=30 -THREADS=1 -KGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELEXT=7
                                                                                                                                                                                    (without alignments)
872.955 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications NA:*

| cgn2_6/ptodata/2/pubpna/DCT_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/DCT_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_PUBGNB.seq:*
| cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US08_PUBGOMB.seq:*
| cgn2_6/ptodata/2/pubpna/US08_PUBGOMB.seq:*
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| cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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                                                                                                                                                        August 16, 2004, 01:12:59; Search time 326 Seconds
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                         OM protein - nucleic search, using frame plus p2n model
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Ygapext 60.0
Fgapext 7.0
Delext 7.0
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58
1 MKIFIFVFIMALILAM
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Maximum DB seq length: 200000000
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Match Length DB
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Xgapop 60.0 , X
Ygapop 60.0 , Y
Fgapop 6.0 , F
Delop 6.0 , D
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Sequence:
                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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Gaps:
                           Sequence 1, Application US/10079754A
Publication No. US20020164625A1
GENERAL INFORMATION:
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100.00%
100.00%
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-10-079-754A-4
               US-10-079-754A-1
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                                                                                                                                                                                                                                                                                1 MetLysIlepheilePheValPheileMetAlaLeuileLeuAlaMetileArgAlaAsp 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 200, Application US/10079623

Sequence 200, Application US/10079623

Sublication No. US20020169302A1

GENERAL INFORMATION:

APPLICANT: Harvikala, 11kka J.

APPLICANT: Grigor, Murray R.

APPLICANT: Grigor, Murray R.

APPLICANT: Molenaar, Adrian J.

ITLE OF INVENTION: Compositions isolated from bovine

ITLE OF INVENTION: mammary gland and methods for their use.

FILE REPERBENGE: 11000.1044c3

CURRENT APPLICATION NUMBER: US/10/079,623

CURRENT FILING DATE: 2002-02-19

NUMBER OF SEQ ID NOS: 370

SEQ ID NO 200

SEQ ID NO 200

LENGTH: 267
                                                                                                                               267
58
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                US-10-079-754A-10 (1-58) x US-10-079-754A-15 (1-267)
; SOPTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 15; LENGTH: 267
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Query Match:
                                                  TYPE: DNA
CRGANISM: Bovine
US-10-079-754A-15
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ORGANISM: Bovine
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US-10-079-623-200
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Pred. No.:
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Pred. No.:
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21 SerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyrPheGlnGln 40
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GURLEALL IN CACTAION:

APPLICANT: Glenn, Matthew
APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Bavis, Stephen R.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
FILE REPERENCE: 11000.1068
CURRENT APPLICATION NUMBER: US/10/079,754A
CURRENT APPLICATION NUMBER: US 09/699,146
PRIOR PILING DATE: 2000-10-27
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-23
PRIOR FILING DATE: 1999-10-33
PRIOR APPLICATION NUMBER: US 60,150,330
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 1
LENGTH: 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USEQUENCE 4, Application US/10079754A; publication No. US20020164625A1; bublication No. US20020164625A1; bublication No. US20020164625A1; general information: US20020164625A1; general information: Murray R. APPLICANT: Glaun, Murray R. APPLICANT: Molenaar, Adrian J. APPLICANT: Molenaar, Adrian J. APPLICANT: Davis, Stephen R. ITILE OF INVENTION: Mammary Gland and Methods for Their USFILE OF INVENTION: Mammary Gland and Methods for Their USFILE OF INVENTION: WUMBER: US/10/079,754A; CURRENT APPLICATION NUMBER: US/10/079,754A; CURRENT FILING DATE: 2002-02-19; PRIOR APPLICATION NUMBER: US 60,162,701; PRIOR APPLICATION NUMBER: US 60,162,701; PRIOR APPLICATION NUMBER: US 60,162,701; PRIOR PELING DATE: 2000-08-22; PRIOR FILING DATE: 2000-08-22; PRIOR PILING DATE: US 60,150,330
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Matches:
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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Query Match:
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ORGANISM: Bovine
                                             TYPE: DNA ORGANISM: Bovine
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                                                               US-10-079-754A-4
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PhelleMetalaLeulleLeualaMetlleArgalaAspSerSerGluGluLysArgHis 27

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43 ATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGCCATGATTAGAGCTGAT 102
                                                                     170 ITCAITAIGGCICTCATCCIAGCCAIGAITAGAGCIGAITCAICTGAAGAGAAACGICAC 229
                                          28 ArglysArglysHisHisHisArgGlyTyrPheGlnGlnTyrGlnProTyrGlnArgTyr 47
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                                                                                                                                                                                                           RESULT 6

Sequence 6, Application US/10079754A

Sequence 6, Application US/10079754A

Publication No. US20020164625A1

GENERAL INFORMATION:

APPLICANT: Grigor, Marray R.

APPLICANT: Grigor, Marray R.

APPLICANT: Molenaar, Adrian J.

APPLICANT: Molenaar, Adrian J.

TITLE OF INVENTION: Compositions Isolated from Bovine

TITLE OF INVENTION: Compositions Isolated from Bovine

TITLE OF INVENTION: Mammary Gland and Methods for Their Use

TITLE OF INVENTION: WINNER: US/10/079,754A

CURRENT PILING DATE: 2002-02-19

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 1999-10-29

PRIOR APPLICATION NUMBER: US 60,162,701

PRIOR APPLICATION NUMBER: US 60,162,701

PRIOR APPLICATION NUMBER: US 60,150,330

PRIOR FILING DATE: 1999-08-22

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FASTSEQ for Mindows Version 4.0
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Mismatches:
Indels:
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Matches:
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US-10-079-754A-3
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DB:
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26

46 ArgTyrProLeuAsnTyrProProAlaTyrPro

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93 TICATTARGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAAAGGTCAC 152
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US-10-10/3-25-45-3

Dublication No. US2002016462541

JOBNEARL INPORMATION:

APPLICANT: Grigor, Murray R.

APPLICANT: Grigor, Murray R.

APPLICANT: Grigor, Murray R.

APPLICANT: Davis, Stephen R.

TITLE OF INVENTION: Compositions Isolated from Bovine

TITLE OF INVENTION: Compositions Isolated for Their Use

TITLE OF INVENTION: Mammary Gland and Methods for Their Use

FILE REFERENCE: 11000.1068

CURRENT APPLICATION NUMBER: US/10/079,754A

CURRENT APPLICATION NUMBER: US 09/699,146

PRIOR PILING DATE: 2000-10-27

PRIOR PILING DATE: 1999-10-29

PRIOR PILING DATE: 1999-10-27

PRIOR PILING DATE: 1999-08-22

PRIOR APPLICATION NUMBER: US 60,162,701

PRIOR APPLICATION NUMBER: US 60,162,701

PRIOR APPLICATION NUMBER: US 60,162,701

PRIOR PILING DATE: 1999-08-23

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 5

LENGTH: 96

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LENGTH: 96
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Matches:
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Matches:
Conservative:
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PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR FILING DATE: 1999-10-29
PRIOR PILING DATE: 1999-10-29
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 AGGAAACGGAAAAAACATCAT 173
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Query Match:
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ORGANISM: Bovine
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ORGANISM: Bovine
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Pred. No.:
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Sequence 48, Application US/09812350
; Dublication No. US20020053097A1
; Publication No. US20020053097A1
; General InfoRMATION:
   APPLICANT: Lindquist, Susan
; APPLICANT: Queitsch, Christine
; APPLICANT: Vierling, Elizabeth
; TITLE OF INVENTION: Transgenic Plants Containing Heat Shock Protein
; FILE REPERENCE: P01979US2
; CURRENT PILING DATE: 2001-03-20
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,769
; PRIOR APPLICATION NUMBER: US 60/190,769
; PRIOR APPLICATION NUMBER: US 60/190,16
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 60/199,116
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 48
; SEQ ID NO 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-918-995-8815
) Sequence 8815, Application US/09918995
) Publication No. US20030073623A1
) GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVEXTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVEXTION: PROW VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/916, 995
CURRENT FILING DATE: 2001-07-30
PRIOR PPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
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Matches:
Conservative:
Mismatches:
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25 CGATATCCACTAAATTATCCTCCTGCGTATCCA 57
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SOFTWARE: FractSEQ for Windows Version 3.0
SEQ ID NO 8815
LENGTH: 181
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; LOCATION: (1)...(181)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-8815
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US-09-812-350-48
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Best Local Similarity:
                                                RESULT 9
US-09-812-350-48/c
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APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT RELIGHTON NUMBER: US/09/918,995
CURRENT RILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR PILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 8118
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US-10-437-963-56029
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Mismatches:
               US-10-079-754A-10 (1-58) x US-09-918-995-8225 (1-390)
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Publication No. US20040123343A1
GENERAL INFORMATION:
                                                                           10 MetalaLeuIleLeuAlaMetIle 17
                                                                                                                                                                                                                                                 Sequence 8118, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | NAME/KEY: misc_feature
| LOCATION: (1) ... (464)
| OTHER INFORMATION: n = A,T,C or G
US-09-918-995-8118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bulkharov, Andrey A.
APPLICANT: Barbazuk, Brad
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-437-963-56029/c
                                                                                                                                                                                                  RESULT 13
US-09-918-995-8118
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Should Should
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
TITLE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/218,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8225
LENGTH: 3990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-079-754A-10 (1-58) x US-10-424-599-92870 (1-339)
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Matches:
Conservative:
Mismatches:
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ORGANISM: Glycine max
FETURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_54877C.1
US-10-424-599-92870
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Mismatches:
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                                                                                                                    10 MetAlaLeuIleLeuAlaMetIle 17
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Publication No. US20030073623A1
GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-09-918-995-8225
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-10-424-599-92870/c
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RESULT 15
US-10-198-846-5963/C
Sugarance 5963, Application US/10198846
Publication No. US2003009974a1
Publication No. US2003009974a1
Publication No. US2003009974a1
GENERAL INFORMATION:
APPLICANT: Lilla, James
APPLICANT: Wang, Youzhen
APPLICANT: Steinman, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: POR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: WOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: USONER: US/10/198,846
CURRENT FILLING DATE: 2002-07-18
PRIOR PRIOR PELING DATE: 2001-07-18
PRIOR PILLING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO S963
LENGTH: 870
TYPE: DNA
ORGANISM: Homo sapiens
FAATURE:
NAME/KEY: misc feature
LOCATION: 768, 779, 781, 785, 800, 804, 809, 811, 821, 823, 829, 10CATION: 768, 779, 781, 785, 800, 804, 809, 811, 821, 823, GUING-10-198-846-5963
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            Length:
Matches:
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Mismatches:
Indels:
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Matches:
Conservative:
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Indels:
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Alignment Scores:
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US-10-079-754A-10 (1-58) x US-10-198-846-5963 (1-870)

Percent Similarity: Best Local Similarity: Query Match: DB:

Search completed: August 16, 2004, 02:01:13 Job time : 329 secs

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Sequence

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Sequence 13, Appl
Sequence 7127, Ap
Sequence 3464, Ap
Sequence 6911, Ap
Sequence 6, Appli
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Sequence 522, Appli
Sequence 6, Appli
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Sequence 146, Ap
Sequence 144, Ap
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CAMPUTE: 1,063

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

COPERATING SYSTEM: PC-DCS/MS-DCS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/415,818

FILING DATE: US/08/415,818

PRICK APPLICATION DATA:

APPLICATION NUMBER: 08/383,746

FILING DATE: 03-FEB-195

ATFORNEY/AGBNT INFORMATION:

NAME: APPOLIATION NUMBER: 34,087
                                     Sequence 12, Application US/08415818
September 12, Margaret A. ApplicaNT: Innemeyer, David L. APPLICANT: Shider, Lin-Lin APPLICANT: Shider, Lin-Lin APPLICANT: Strader, Carherine D. APPLICANT: Tan, Carina P. APPLICANT: Tan, Carina P. APPLICANT: Wellnergy David H. TITLE OF INVENTION: NEUROPERTIDE Y RECEPTOR NUMBER OF SEQUENCES: 12 CORRESPONDENCE MAD NA. Appolling STREET: P.O. Box 2000, 126 E. Lincoln Ave. CITY: Rahway STATE: NJ SA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA CITY: NAME OF STATE OF STAT
RESULT 1
US-08-415-818-12
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-MODEL=frame+ n 12p model - DEV-xlp
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-G=/CGN12_1/USFTO_spool_p/US10079754/runat_06082004_180756_1._LOOPCL=0
-DB=Issued Patents AA - QEMT=fastan - SUFFIX=rai - MINMATCH=0.1 - LOOPCL=0
-LOOPEXT=0 - UNITS=bits - START=1 - STND=1 - MATRX=bloom62 - TRANS=human40.cdi
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-MODE=LOCAL_OUTFWT=pto - NORMeext - HEAPSIZE=500 - MINLEN=0 - MAXLEN=200000000
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-DEV_TIMEOUT=120 - WARN_TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
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Sequence 12, Appl
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Sequence 4, Appli
Sequence 6, Appli
Sequence 1981s, Appli
Sequence 1981s, Appli
Sequence 5672, Appli
Sequence 27, Appli
Sequence 27, Appli
                                                                                                                                                                     August 6, 2004, 17:10:01; Search time 22 Seconds (without alignments) 2834.735 Million cell updates/sec
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   /C9Ta_6/prodata_2/iaa/5B_COMB.pep:*
3: /C9Ta_6/prodata_2/iaa/6A_COMB.pep:*
4: /C9Ta_6/prodata_2/iaa/6B_COMB.pep:*
5: /C9Ta_6/prodata_2/iaa/FB_COMB.pep:*
6: /C9Ta_6/prodata_2/iaa/PCTUS_COMB.pep:*
6: /C9Ta_6/prodata_2/iaa/PCTUS_COMB.pep:*
                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-495-714C-6

US-09-495-714C-6

US-09-252-991A-19818

US-09-252-991A-19818

US-08-936-165A-395

US-08-107-532A-5672

US-08-159-340A-25

US-08-286-819A-25
                                                                                                                          OM nucleic - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Maximum Match 100%
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Ygapop 10.0 , Ygapext
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Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Perfect score:
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Database :

Result

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370 amino acids
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35.51%
22.90%
7.23%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                 STREET: P.O. CITY: Rahway
                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                  STATE: NJ
COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 TyrThrHisGlnValAlaCysValGluAsnTrp-----ProSerLysLysAspArgLeu 207
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139 ValAsnProArgGlyTrpLysProSerValThrHisAlaTyr----------
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|SerLeuLeuLeuSerIleProPhePheLeuSerTyrHisLeuThr-------
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Mismatches:
Indels:
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Matches:
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Patent No. 5939263
GENERAL INFORMATION:
APPLICANT: Cascieri, Margaret A.
                                              TELEFAX: 908-594-4720
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acid
STRANDEDNESS: single
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3462
                                                                                                                                                                                                                                  0.892
75.00
35.51%
22.90%
7.23%
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MOLECULE TYPE: protein
US-08-415-818-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                      510 TCA-----
                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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429 -----TTATTCATTTGAAAGATGGTTTTCAACACAAAAAGAGAGAAAAATC 379
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Mary A. Appollina
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
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FILING DATE:
CLASSIPICATION DATA:
CLASSIPICATION DATA:
APPLICATION UNDER: US/08/694,236
APLICATION UNDER: 06/383,746
FILING DATE: 03-FEB-1995
PRIOR APPLICATION UNDER: 06/415,818
FILING DATE: 03-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: APPOLITION:
NAME: APPOLITION
REFERENCE/DOCKET NUMBER: 19390Y
TELECHANNICATION NUMBER: 19390Y
TELECHANNICATION INFORMATION:
APPLICANT: Linemeyer, David L.
APPLICANT: MacNeil, Douglas J.
APPLICANT: Shiao, Lin-Lin
APPLICANT: Stader, Catherine D.
APPLICANT: Tan, Carina P.
APPLICANT: Weinberg, David H.
TITLE OF INVENTION: NEUROPEPTIDE Y RENUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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463

STRANDEDNESS: single i TOPOLOGY: linear i MOLECULE TYPE: protein pcT-US96-01444-12 Alignment Scores: 0.892	10-079-754A-4 (1-604) x PCT-US96-01444-12 (1-370)	Qy 564 ATGGTAAGTGACAGAGAAAGAAAGTAAATTAGAAT	Oy 510 TCATATTATGTTTTAAAATTTGATATTTG 	Oy 462 TGCAACTACTTGACTG	Qy 429TIATICALITGAAAGAIGGITTICAACACAACAG (2)	378 A	Db 139 ValAsnProArgGlyTrpLysProSerValThrHisAlaTyr-	153	Qy 273 TIGTTGAAAATAICCTCTAIGATGTTTTTCCGTTTCCTGTGA ::: ::: :::	מ מ		HisGlnValAlaCysValGluAsnT	Qy 120 CTGATGCTTCAGGAGATGTTCTTGCTAGAAAACTGCTGTGTT	Qy 60 TTCATTTGTAATTACATCAGTTATGAGATCTTATTA	RESULT 4 US-09-495-714C-2 Sequence 2, Application US/09495714C Patent No. 6670465 GENERAL INCORMATION: PAPLICANT: University Technologies International Inc. PILLE OF INVENTION: RETINAL CALCUU GENNEE (ALPHA) 11F FILE REFERENCE: 45499-4 (formerly 45074.6) CURRENT PRILING DATE: 2000-02-01 NUMBER OF SEQ ID NOS: 138 SOFTWARE: PatentIn version 3.1 SEQ ID NO 2.2	י דביו יידי יידי יידי יידי יידי יידי ייד
::: 139 ValasnProArgGlyTrpLysProSerVa 330 TraAgGaAATGGATAGGAGGAGATAAT 153	177AspGluProPheHisAsnLeuSerLeuProThrAspLeu	Qy 156 CATATT	Qy 120 CTGATGCTTCAGGAGATGTTCTTTGCTAGAAAACTGCTGTTTAAATACCTTGAAATCC 61	OY 60 TICATITGIAATIACATCAGTIAIGAGAICTIAITA 19	RESULT 3 PCT-US96-01444-12	삼弦	** APPLICANT: Intemedyer, David L. APPLICANT: MacNeil, Douglas J. APPLICANT: Shiae, Lin-Lin	Strader, Catherine D. Tan, Carina P. Weinberg, David H.	; TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR ; NUMBER OF SEQUENCES: 14 ; CORRESPONDENCE ADDRESS:	ю. н	; STATE: NJ COUNTY USA ; ZIP: 07065	; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible) OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: Patentin Release #1.0, Version #1.30 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: PCT/US96/01444	; FILING DATE: ; CLASSIFICATION: ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: 08/383.746	FILING DATE: 03-FEB-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/415,816 FILING DATE: 03-APR-1995 ATTORNEY/AGENT INFORMATION: NAME: APPOILING, MARY A. REGISTRATION NUMBER: 34,087 REFERENCE/DOCKET NUMBER: 19390Y TELEPHONE: 908-594-7662 TELEPHONE: 908-594-726 INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 370 amino acids LENGTH: 370 amino acids	; TYPE: amino acid

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AGTCATGAAAGATGAAATT 121
                                                                                                                                                                                                               ATCGTTGATATGGCTGGTA 274
                                                                                                                                                                                                                                                                                                                      uSerLeuProThrAspLeu 189
                                                                                                                            AGAAAGAGTAGGAAAAATC 379
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|GluArgTyrGlnLeuIle 138
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|uThr----- 176
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                                                                                 IGATTTTTTTTTTGTT 430
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rSerTyrValGlnSerVal 118
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TTACATAGTTCAGAGACTA 511
                                        GATICCAAGIAIGIGITG 463
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rileLeuIleAlaAsnLeu 78
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1F-SUBUNIT GENE
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TYPE: PRT ORGANISM: Mus musculus
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Best Local Similarity:
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US-09-495-714C-6
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                    GAGAGCCATAATGAAGACAAAGATAAAGAT---------CTTCATATTTGG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                        561 GlyProPhePheProGlyMetLeuValCysIleTyrPheIleIleLeuPheIleCys--- 679
                                                                                                                                                                                                                                               -------TGGAGTCCAGTCATGAAAATTCTGATGCTTCAG 109
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Patent No. 6670465

GENERAL INFORMATION:
TITLE OF INVENTION: RETINAL CALCIUM CHANNEL (ALPHA) IF-SUBUNIT GENE
FILE REFERENCE: 45499.4 (formerly 45074.6)
CURRENT APPLICATION NUMBER: US/09/495,714C
CURRENT FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 138
SOFTWARE: Patentin version 3.1
LENGTH: 1977
                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Gaps:
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                                                                                                                            Gaps:
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73.50
42.31
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42.31%
24.62%
7.09%
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-495-714C-2
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Best Local Similarity:
Query Match:
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686 GlnThrHisThrLysArgSerThrPheAspThrPheProGlnAlaLeuLeuThrValPhe 705
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                                                                                                                                                                                                                                                                                                                                                         108 GAGATGTTCTTTGCTAGAAACTGCTGTGTTTAAATACCTTGAAATCCTTCATTTGTTTT 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09495714C
Patent No. 6670465
GENERAL INFORMATION:
TILLE APPLICANT: University Technologies International Inc.
TILLE OF INVENTION: RETINAL CALCIUM CHANNEL (ALPHA) IF-SUBUNIT GENE FILE REPERENCE: 45499.4 (formerly 45074.6)
CURRENT APPLICATION NUMBER: US/09/495,714C
CURRENT FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 138
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1985
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Mismatches:
Indels:
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                                                                                                                          677 LeuPheGlyGlyLysPheAsnPhe--------
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                        48 TGTAATTACATCAGTTATGAGATCTTATTA 19
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72.50
42.31%
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225 uSerPheLeu 228
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Best Local Similarity:
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US-08-936-165A-395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
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ThrPheLeuSerGluGluArgLeuLysLeuGlnAlaProLeuVallleArgLeuGlyGln 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 IleThrGluSerGlyGlnTrpAsn-MetSerGlyAsnAspValCysAsnPheArgValLe 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          425 AATAAAACAAAAAAAAAAATCAGTCAAGTAGTTGCACAACATACTTGGAATCAAAT 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::: :::||| ||| ||| LysGluValArgLysAspProSerGluGluSerGluGluAsnThrGlyIleGluProAsn 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      502
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                                   GAGATGTTCTTTGCTAGAAACTGCTGTGTTTAAATACCTTGAAATCCTTCATTTGTTTT 49
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                  Sequence 176, Application US/09489847

Patent No. 6476195

GRUERAL INFORMATION

APPLICANT: Rosen et al

TITLE OF INVENTION: 98 Human Secreted Proteins

FILE REFERENCE: PO20191

CURRENT APPLICATION NUMBER: US/09/489,847

CURRENT FILING DATE: 1099-07-29

EARLIER FILING DATE: 1999-07-29

EARLIER PILING DATE: 1998-07-29

EARLIER APPLICATION NUMBER: 60/094,657

EARLIER APPLICATION NUMBER: 60/096,319

EARLIER APPLICATION NUMBER: 60/095,486

EARLIER PILING DATE: 1998-08-05

EARLIER PILING DATE: 1998-08-05

EARLIER FILING DATE: 1998-08-06

EARLIER PILING DATE: 1998-08-06

EARLIER PILING DATE: 1998-08-06

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: SITE
LOCATION: (233)
COTATE NIFFER INFORMATION: Xaa equals stop translation
US-09-489-847-176
                                                                                                                                485 ATCAATATTTAAAACAT---------
                                                                                                    TGTAATTACATCAGTTATGAGATCTTATTA
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70.00
43.27$
24.04$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                        -09-489-847-176
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## Sequence 1991A-19818

| Sequence 1991B, Application US/09252991A | Sequence 1991B, Application US/09252991A | Sequence 1991B, Application US/09252991A | Sequence 1991B, Application General No. 6551795 | Sequence 1991B-1995 | Sequence 1991B
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164 ThrMetAsnLeuLysGlnGluHisLeuArgAsnAlaProGlyLeuAspLysValLeuTyr 183
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70 SerThrSerValLeuAlaThrValProLeuArgSerSerGluThrAlaArg1leLeuPro
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184 AspAsniysLeuAspValValGlnArgAlaLeuGlyLeu 196
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Matches:
Conservative:
Mismatches:
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US-09-252-991A-19818
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Sequence 5672, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::: :::::: ||||||| :::||||:::
167 GlnAsnLeuLysPheAsnTyrLysMetGlnGlnTyrTyrPheValPheThrLeuIlePhe 186
                                            |||::
-----PheIleAlaIl 111
                   105 ATGITCTTTGCTAGAAAACTGCTGTGTTTAAATACCTTGAAATCCTTCATTTGTTTTTGT 46
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31
441
72
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                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           546 AAGAAAGTAGAAACCAATTACATAGTTCAGAGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/081571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 40,489
                                                                                                                                           111 eLeuThrLeuThrMetTrpSerGluTyrArg 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...482
SEQUENCE DESCRIPTION: SEQ ID NO: 5672:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                        45 AATTACATCAGTTATGAGATCTTATAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 482 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5672:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.00
43.54%
21.09%
6.56%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                            US-09-107-532A-5672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCTTCAGATGAATCAGCTCTAATCATGGCTAGGATGAGAGCCATAATGAAGACAAAGAT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 AAAGATCTTCATATTTGGTGGAGTCCAGTCATGAAAGATGAAATTCTGATGCTTCAGGAG 106
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LysArgValHis---------ArgHisAlaLeuIleLeuPheValAla 103
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61 IleTrpSerAsnPheIleGluMetGlySerMetLeuLeuProMetSerMetLeuPhe 80
                                                                                                                                                                                                                                                                        TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides, TITLE OF INVENTION: Polypeptides and Their Uses NUMBER OF SEQUENCES.

CORRESPONDENCE ADDRESS:
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OCHROLLER: LD: COMPACTATION OF SECURIOR SOFTWARE: | FRAESEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/936,165A FILING DATE: 24-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REGISTRATION NUMBER: 950549
TELEPONATION INFORMATION:
TELEPHONE: 610-270-4478
TELEPHONE: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-079-754A-4 (1-604) x US-08-936-165A-395 (1-273)
                                                                                                                                                                                                                                                                                                                                                          SEE: SmithKline Beecham Corporation
: 709 Swedeland Road
King of Prussia
    Application US/08936165A
                                                                                    Burnham, Martin
Hodgson, John
Knowles, David
Lonetto, Michael
Nicholas, Richard
Pratt, Julie
Reichard, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 395:
                                                                                                                                                                                                                                       Rosenberg, Martin
Ward, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: ......
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
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25.27%
6.61%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Sequence 395, Appli
Patent No. 6348582
GENERAL INFORMATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-936-165A-395
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                STREET: 7
CITY: Kir
STATE: PP
COUNTRY:
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APPLICANT:
APPLICANT:
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Matches:

926

Length:

9.1

Alignment Scores: Pred. No.:

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RESULT 12
US-08-286-819A-25
Sequence 25, Application US/08286819A
APPLICANT: MOLINAS, CATHERINE
APPLICANT: OULY ALLIA PATRICE
TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPRETIDES, IN PARTICULAR
TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLECTIDE SEQUENCE CODING FOR
TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESSE: P.C. 165
ADDRESSER: P.C. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      489
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515 nLeu------AsnMetAsnSerAsnGlyHisSerSerAlaThrSerThrileGl 531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Alloquon
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: DAVE FOR PC-DOS/MS-DOS
SOFTWARE: Parentin Release #1.0, Version #1.25
CURRENT ARRENT ADDRA:
APPLICATION NUMBER: US/08/286,819A
     222
101
101
101
                          Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                 133 CATGACTCCACCAAATATGAAG------
                                                                                                                                                                US-10-079-754A-4 (1-604) x US-08-159-340A-2 (1-926)
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67.50
39.11%
26.82%
6.56%
                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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91 TCTAGCAAAGAACATCTCCTGAAGCATCAGAATTTCATCTTTCATGACTGGACTCCACCA 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 AATAIGAAGAICITIAICITIGICITICATIAIGGCICICACCIAGCCAIGAIT 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161
21
8
18
11
                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-079-754A-4 (1-604) x US-08-980-357-25 (1-161)
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/200,337
FILING DATE:
RIGHT APPLICATION DATA:
APPLICATION NUMBER: US 08/286,819
FILING DATE: 05-A0G-1994
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
PRIOR APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992
PRIOR APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 39-OCT-1991
PRIOR APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 31-OCT-1991
APPLICATION NUMBER: PR 9013579
FILING DATE: 31-OCT-1990
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 24,618
RESERRENCE/DOCKET NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 60, Application US/09393634
Patent No. 6558910
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zuker, Charles S. APPLICANT: Adler, Jon Elliot APPLICANT: Ryba, Nick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELERX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 161 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 161 amino acids
amino acid
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66.50
50.00%
36.21%
6.46%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                       Virginia
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-393-634-60
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Sequence 25, Application US/08980357

Patent No. 601328

Patent No. 601328

Patent DUKTN-AMLEN, SILVIE

APPLICANT: DUKTN-AMLEN, SYLVIE

APPLICANT: OCHRVALIN PARRICE

TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR

TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS

TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.

STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 ileThrAspValileThrAsnThrValGlyGlyPheLeuGlyLeuLysLeuTyrGlyLeu 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTAGCAAAGAACATCTCCTGAAGCATCAGAATTTCATCTTTCATGACTGGACTCCACCA 150
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-079-754A-4 (1-604) x US-08-286-819A-25 (1-161)
                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER:

CLASSIFCATION:
APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-MG-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: F 9013579
FILING DATE: 31-OCT-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPRAX: (703) 413-3000
TELEFRAX: (703) 413-3000
  05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 161 amino acids
amino acid
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66.50
50.00%
36.21%
6.46%
FILING DATE: 05-AUG-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-286-819A-25
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MEDIUM TYPE:
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DB:
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51    LeuAlaIleSerArgIleSerLeuValTrpLeuIlePheGlySerTrpCysValSerVal
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APPLICANT: Mueller, Ken
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
FILE REPERENCE: 02307E-09800008
CURRENT APPLICATION NUMBER: US/09/393,634
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 60
TUNION FOR THE OFFICE OFFICE
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APPLICANT: Hogeveen, Ron C.
APPLICANT: Hogeveen, Ron C.
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
TITLE OF INVENTION: UPCTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 229
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
STREET: P.O. Box 4433
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US-09-393-634-60
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US-09-079-030-219
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Mismatches:
Indels:
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Matches:
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Job time : 27 secs
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APPLICATION NUMBER: US/09/079,030
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Sequence 6, Appliscoquence 6, Appliscoquence 246, Appliscoquence 147146, Sequence 103, Appliscoquence 103, Appliscoquence 103, Appliscoquence 54218, Appliscoquence 5221, Appliscoquence 1927, Appliscoquence 193953, Sequence 63502, Appliscoquence 63502, App
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Sequence 52793, A
Sequence 127400,
Sequence 395, App
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APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Molemaar, Adrian J.
APPLICANT: Molemaar, Adrian J.
APPLICANT: Mammary Gland and Methods for Their Use TITLE OF INVENTION: Compositions Isolated from Bovine
FILE OF INVENTION: Mammary Gland and Methods for Their Use FILE REFERENCE: 11000.1068
CURRENT APPLICATION NUMBER: US/10/079,754A
CURRENT FILING DATE: 2002-02-19
PRIOR PILING DATE: 1999-10-29
PRIOR PILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR FILING DATE: 1999-08-22
PRIOR FILING DATE: 1999-08-22
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
3 US-10-079-754A-7
3 US-10-079-754A-10
3 US-10-079-754A-10
3 US-10-079-754A-10
3 US-10-079-754A-9
3 US-10-079-754A-9
3 US-10-079-754A-9
3 US-10-079-754A-9
3 US-10-10-172-168
0 US-09-992-600A-6
0 US-09-992-600A-6
0 US-09-992-095B-6
0 US-09-992-147146
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0 US-09-993-147146
0 US-09-993-1534-1761
2 US-10-437-963-193953
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0 US-09-510-332-131
2 US-10-424-599-156448
2 US-10-282-122A-63523
2 US-10-424-599-159483
2 US-10-282-122A-7323
2 US-10-424-599-159483
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US-10-335-977-7067
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US-10-079-754A-7
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-MODEL=frame+ n2p,model - DEV=Xlp
-MODEL=frame+ n2p,model - DEV=Xlp
-MODEL=frame+ n2p,model - DEV=Xlp
-Q=/cgn2 1/USFO spool D/US10079754/runat_06062004_180758_1746/app_query.fasta_1.775
-D=Published Applications AA - CFMT=fastan - SUFFIX=rapb - MINNATCH=0.1
-LOOPCL=0 - LOOPEXT=0 - UNITS=bits - START=1 - END=-1 - MATRIX=blosum62
-TRANS=human40.cdi - LIST=45 - DOCALIGN=200 - THR_SCORE=pct - THR_MAX=100
-MAXIEN=200000000 - USR=-BIGOT-OUTFMP=0 - NORM-ext - HEAPSIZE=500 - MINLEN=0
-MAXIEN=200000000 - USR=-BIGOT-OUTFMP=0 - NORM-ext - HEAPSIZE=500 - MINLEN=0
-MAXIEN=200000000 - USR=-BIGOT-OUTFMP=0 - NORM-ext - HEAPSIZE=500 - MINLEN=0
-NORM-G - CICPU=3 - NO_MMAP - LAGREQUERY - NEG SCORES=0 - WAIT - DSPBLOCK=100
-LONGLOG - DEV TIMEOUT=120 - WARN TIMEOUT=30 - THRREADS=1 - XGAPOR=10 - XGAPEXT=0.5
-FGAPOR=6 - FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
                                                                                                                                                                                                       August 6, 2004, 17:14:11; Search time 48.5 Seconds (without alignments) 7812.969 Million cell updates/sec
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1 gaagtattttcagttctata......tatcaagcataaaaaaaa 604
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUBL_pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUBL_pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
                                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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Maximum DB seq length: 2000000000
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US-10-079-754A-10

US-10-079-754A-10

Sequence 10, Application US/10079754A

Publication No. US20020164625A1

GENERAL INFORMATION:

APPLICANT: Grigor, Murray R.

TITLE OF INVENTION: Compositions Isolated from Bovine

TITLE OF INVENTION: Mammary Gland and Methods for Their Use

FILE REFERENCE: 11000 1068

CURRENT APPLICATION NUMBER: US/10/079,754A

PRIOR FILING DATE: 2002-02-19

PRIOR FILING DATE: 2000-10-27

PRIOR PLICATION NUMBER: US 60,162,701

PRIOR FILING DATE: 2000-08-22

PRIOR PLICATION NUMBER: US 60,162,701

PRIOR PLICATION NUMBER: US 60,162,701

PRIOR FILING DATE: 1999-10-29

PRIOR PLICATION NUMBER: US 60,150,330

PRIOR FILING DATE: 1999-08-23

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10

LENGTH: 58

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LENGTH: 58
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Query Match:
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Percent Similarity:
Best Local Similarity:
; SEQ ID NO 7
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Bovine
US-10-079-754A-7
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; ORGANISM: Bovine
US-10-079-754A-10
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274 TACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTATCCATTTCCT 327
                                                                                     RESULT 3
US-10-079-754A-B
Sequence 8, Application US/10079754A
Publication No. US20220164625A1
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Grigor, Muray R.
APPLICANT: Grigor, Muray R.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: LONGOSITION REMAINSTRY BEILNG DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 09/699,146
PRIOR APPLICATION NUMBER: US 09/699,146
PRIOR APPLICATION NUMBER: US 00,162,701
PRIOR PILING DATE: 1099-10-29
PRIOR PILING DATE: 1099-10-29
PRIOR PILING DATE: 1099-10-29
PRIOR PILING DATE: 1099-10-29
PRIOR PILING DATE: 1999-08-23
PRIOR PILING DATE: 1999-08-23
PRIOR PILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEC ID NOS: 15
SOFTWARE: FESTSEQ for Windows Version 4.0
LENGTH: 58
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Publication No. US20020164625AI
GENERAL INPORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Molennar, Adrian J.
APPLICANT: Molennar, Adrian J.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
FILE REFERENCE: 11000.1068;
CURRENT APPLICATION NUMBER: US/10/079,754A;
CURRENT FILING DATE: 2002-02-19
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CRGANISM: Bovine
US-10-079-754A-8
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US-10-079-754A-12
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publication No. US20020164625A1

publication No. US20020164625A1

publication No. US20020164625A1

APPLICANT: Glenn, Matthew

APPLICANT: Grigor, Murray R.

APPLICANT: Molenaar, Adrian J.

PRICA INVENTION: Compositions Isolated from Bovine

TITLE OF INVENTION: Compositions Isolated from Bovine

TITLE OF INVENTION: Momber: US/10/079,754A

CURRENT APPLICATION NUMBER: US 09/699,146

PRIOR FILING DATE: 2000-10-27

PRIOR PRILOR DATE: 2000-10-27

PRIOR APPLICATION NUMBER: US 09/644,190

PRIOR APPLICATION NUMBER: US 09/644,190

PRIOR APPLICATION NUMBER: US 60,150,330

PRIOR APPLICATION NUMBER: US 60,150,330

PRIOR PLING DATE: 1999-10-29

PRIOR PRILOR PRILOR WINDER: US 60,150,330

PRIOR PRILOR PRILOR WINDER: WINDER:
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PRIOR APPLICATION NUMBER: US 09/699,146
PRIOR FILING DATE: 2000-10-27
PRIOR PLILING DATE: 2000-10-27
PRIOR PLILING DATE: 1998-10-29
PRIOR FILLING DATE: 1998-10-29
PRIOR FILLING DATE: 2000-08-22
PRIOR FILLING DATE: 2000-08-22
PRIOR FILLING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTESEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 59
TYPE: PRI
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Pred. No.:
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APPLICANT: Glenn, Matthew
APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Mammary Gland and Methods for Their Use TITLE OF INVENTION: Compositions Isolated from Bovine FILE REFERENCE: 11000.1068
CURRENT APPLICATION NUMBER: US/10/079,754A
CURRENT FILING DATE: 2002-02-19
FRIOR APPLICATION NUMBER: US 09/699,146
FRIOR APPLICATION NUMBER: US 09/644,190
FRIOR PILING DATE: 1999-08-23
FRIOR APPLICATION NUMBER: US 09/644,190
FRIOR FILING DATE: 1999-08-23
                                                                                                                                                                                                                                                      214 TCATCTGAAGAAACGTCACAGGAAACGGAAAAAACATCAT 255
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                                                                               US-10-079-754A-4 (1-604) x US-10-079-754A-9 (1-70)
                           Gaps:
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sequence 11, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
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Publication No. US20040043928A1
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Ji, Weizhen
Padigaru, Muralidhara
Casman, Stacie
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APPLICANT: Kekuda, Ramesh
APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles
APPLICANT: Penturajan, Meera
APPLICANT: Pena, Carol
APPLICANT: Rieger, Daniel
APPLICANT: Shimkets, Richard
APPLICANT: Zerhusen, Bryan
APPLICANT: Li, Li
APPLICANT: Ji, Weizhen
APPLICANT: Ji, Weizhen
APPLICANT: Casman, Stacie
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Best Local Similarity:
Query Match:
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US-10-079-754A-11
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Pred. No.:
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US-09-91/-3401.

US-09-91/-3401.

Sequence 19, Application US/09917340

Patent No. US2002009369A1

GENERAL INDORMATION:

APPLICANT: Murphy, Christopher J.

APPLICANT: McAnulty, Jonathan F.

APPLICANT: Reid, Ted W.

TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468

CURRENT APPLICATION NUMBER: 06/9917,340

CURRENT FILING DATE: 2001-07-29

PRIOR APPLICATION NUMBER: 60/249,602

PRIOR PILING DATE: 2000-01-17

PRIOR PLILING DATE: 2000-01-17

PRIOR PLILING DATE: 2000-01-17

PRIOR PLILING DATE: 2001-01-17

PRIOR PLILING DATE: 2001-01-15

NUMBER OF SEQ ID NOS: 96

SEQ ID NOS: 96

SEQ ID NOS: 96

FENNANCE: Patentin Ver. 2.0
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59.57%
46.81%
9.23%
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NUMBER OF SEQ ID NOS: 114
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-992-600A-6
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APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Alsobrook II, John
APPLICANT: Lepley, Denise et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-416
CURRENT APPLICATION NUMBER: US/10/210,172
CURRENT FILING DATE: 2001-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 AIGAAGATCTITATCTTTGTCTTCATTATGGCTCTCATCCTAGCCTGATTAGAGCTGAT 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/329,501
PRIOR PILING DATE: 2001-08-02
PRIOR PLILING DATE: 2001-08-02
PRIOR PLILING DATE: 2001-09-21
PRIOR PLILING DATE: 2001-09-21
PRIOR PLILING DATE: 2001-09-21
PRIOR PLILING DATE: 2001-09-19
PRIOR PLILING DATE: 2001-08-03
PRIOR PLILING DATE: 2001-08-03
PRIOR PLILING DATE: 2001-08-09
PRIOR PLILING DATE: 2001-08-09
PRIOR PLILING DATE: 2001-08-09
PRIOR PLILING DATE: 2001-08-09
PRIOR PLING DATE: 2001-08-09
PRIOR PLILING DATE: 2001-08-13
PRIOR PLILING DATE: 2001-08-17
PRIOR PLING DATE: 2001-08-17
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61.82$
49.09$
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Rastelli, Luca
Spytek, Kimberly
Edinger, Shlomit
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Gerlach, Valerie
                                                                                                                                    Anderson, David
Guo, Xiaojia
                                                                                                                                                                                                                                                                                                                                                           llerman, Karen
Voss, Edward
Boldog, Ferenc
Gorman, Linda
                                                                                                             Vernet, Corine
                                                                                Leite, Mario
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, ORGANISM: Homo sapiens
US-10-210-172-168
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US-0952-600A-6

Sequence 6, Application US/09992600A

Publication No. US20030027161A1

GENERAL INFORMATION:

APPLICANT: Benjanin, Stephane

APPLICANT: Benjanin, Stephane

APPLICANT: Benjanin, Stephane

APPLICANT: Tanaka, Hiroaki

TITLE OF INVENITYON: HUMAN CDNAS AND PROTEINS AND USES THEREOF

FILE PREFERENCE: 91.U54_DIV

CURRENT TILING DATE: 2001-11-13

PRIOR PLING DATE: 2001-10-13

PRIOR PLING DATE: 2001-00-06

PRIOR FILING DATE: 2001-00-13

PRIOR FILING DATE: 2001-00-13

PRIOR FILING DATE: 2001-00-13

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-25

PRIOR FILING DATE: 2001-06-25
                                                                                                                                                                                                                                                                                                                                                  214 TCATCTGAAGAGAAACGTCAC---AGGAAACGGAAAAAAACAT----
  Length:
Matches:
Conservative:
Mismatches:
Indels:
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US-09-999-570-6
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                                                                                                                                                                                                                                                                                                              Sequence (A Application US/09924340)

Publication No: US20030027248A1

Publication No: US20030027248A1

GENERAL INFORMATION:

APPLICANT: Bejanin, Stephane

APPLICANT: Tanaka, Hiroaki

TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

FILE REFERENCE: 91.US2.REC

CURRENT APPLICATION NUMBER: US/09/924,340

CURRENT FILING DATE: 2001.08-06

PRIOR FILING DATE: 2001.07-07-13

PRIOR FILING DATE: 2001.06-13

PRIOR PLICATION NUMBER: US 60/298,698

PRIOR PLICATION NUMBER: US 60/298,698

PRIOR FILING DATE: 2001.06-15

PRIOR FILING DATE: 2001.06-15

PRIOR FILING DATE: 2001.06-15

PRIOR FILING DATE: 2001.06-15

SOFTWARE OF SEQ ID NOS: 112

SEQ ID NO 6

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9.18%
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94.50
56.36%
32.73%
9.18%
                                              TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Best Local Similarity:
                                                                        FEATURE:
NAME/KEY: SIGNAL
LOCATION: 1..19
US-09-992-600A-6
   SOFTWARE: JPatent
SEQ ID NO 6
LENGTH: 78
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; LOCATION: 1..19
US-09-924-340-6
                                                                                                                                                 Alignment Scores:
Pred. No.:
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154 ATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGCCATGATTAGAGCTGAT 213
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214 TCATCTGAAGAGAAACGTCACAGGAAACGGAAAAAACATCATAGAGGATATTTTCAACAA 273
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18-Equence 6, Application US/0992095B

Publication No. US20030157485A1

Publication No. US20030157485A1

GENERAL INFORMATION: Stephane

APPLICANT: Benjain, Stephane

APPLICANT: Benjain, Stephane

APPLICANT: Benjain, Stephane

TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

FILE REFERENCE: 91. US5.DIV

CURRENT APPLICATION NUMBER: US 09/92,095B

CURRENT FILING DATE: 2001-08-06

PRIOR PILING DATE: 2001-08-06

PRIOR PILING DATE: 2001-08-06

PRIOR PILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/305,456

PRIOR PILING DATE: 2001-07-13

PRIOR PILING DATE: 2001-06-29

PRIOR PILING DATE: 2001-06-29

PRIOR PILING DATE: 2001-06-25

PRIOR APPLICATION NUMBER: US 60/293,574

PRIOR PILING DATE: 2001-06-25

NUMBER OF SEC ID NOS: 112

SSPC ID NO 6
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56.36%
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NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
SEQ ID NO 6
LENGTH: 78
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US-10-000-986-6
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TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: G-091US08DIV
CURRENT PELING DATE: 2001-06-14
PRIOR PAPLICATION NUMBER: US/9999,570
CURRENT FILING DATE: 2001-06-14
PRIOR PAPLICATION NUMBER: PCT/1801/01715
PRIOR PAPLICATION NUMBER: PCT/1801/01715
PRIOR PAPLICATION NUMBER: PCT/1801/01715
PRIOR PELING DATE: 2001-08-06
PRIOR PELING DATE: 2001-07-13
PRIOR PELING DATE: 2001-07-13
PRIOR PELING DATE: 2001-06-29
PRIOR PELING DATE: 2001-06-29
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TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.USG.DIV
CURRENT APPLICATION NUMBER: US/10/000,489
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR PLING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
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Publication No. US20030032011A1
GENERAL INFORMATION:
GPPLICANT: Benjanin, Stephane
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ORGANISM: Homo sapiens
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| Sequence 6, Application WS/10000986
| Publication No. US20030096247A1
| GENERAL INFORMATION:
| APPLICANT: Benjamin, Stephane
| APPLICANT: Benjamin, Stephane
| APPLICANT: Tanaka, Hircaki, Hircaki, Hirle OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF FILLS REPERBNEE: 91.US9.DIV
| CURRENT APPLICATION NUMBER: US 09/924,340
| PRIOR PILING DATE: 2001-11-14
| PRIOR PILING DATE: 2001-08-06
| PRIOR PILING DATE: 2001-08-06
| PRIOR PILING DATE: 2001-08-06
| PRIOR PILING DATE: 2001-07-13
| PRIOR PILING DATE: 2001-07-13
| PRIOR PILING DATE: 2001-07-13
| PRIOR PILING DATE: 2001-06-29
| PRIOR PILING DATE: 2001-06-25
| NUMBER OF SEQ ID NOS: 112
| SEQ ID NO 6
| LANGTH OF SEQ ID NOS: 112
| LANGTH: DATE: DATE
| LANGTH: DATE: 2001-06-25
| LANGTH: DATE: 2001-06-25
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ORGANISM: Homo sapiens
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-000-986-6
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154 ATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGCCATGATTAGAGCTGAT 213
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(Sequence 6, Application US/10154678)

Publication No: US20030162186A1

GENERAL INFORMATION:

APPLICANT: Benjanin, Scephane

APPLICANT: Tanaka, Hiroaki

TITLE OF INVENTION: HUPAN CONAS AND PROTEINS AND USES THEREOF

FILE REFERENCE: 182.U51.RG

CURRENT APPLICATION NUMBER: US/10/154,678

CURRENT APPLICATION NUMBER: US 60/305,456

PRIOR FILING DATE: 2001-08-06

PRIOR PLICATION NUMBER: US 60/305,456

PRIOR PLILOATION NUMBER: US 60/305,574

PRIOR PLILOATION NUMBER: US 60/298,698

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15
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ORGANISM: Homo sapiens
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Alsbrocks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J. Bencon, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bunck, J., Bursel, K.L., Bouck, J., Chard, J., Chen, G., Chen, G., Chen, G., Choy, Carroll, L.D. Dederich, David, R., Dalaney, K.R., Dalgado, J., Denn, A.L., Ding, Y., Dinh, H.H., Doulbaick, J., Darger, H., Dugan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Elagg, M., Ford, J., Foster, P., Frantz, P., Garcia, P., Garcia, P., Garcia, P., Haris, C., Harris, K., Hart, M., Ford, J., Foster, P., Frantz, P., Harris, C., Harris, K., Hart, M., Havlak, P., Hamilton, K., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Harnandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Lozado, E., Kursen, B., Land, W., Loudah, S., Karlsson, E., Karlsson, E., Karlston, R., Land, W., Lang, L., Korvah, J., Kovar, C., Karlsson, E., Karlston, R., Land, W., Ming, L., Korvah, J., Loudah, S., Hart, M., Mapue, P., Martindel, M., Martindez, M., Masch, G., Martinder, M., Martinder, M., Masch, G., Marting, E., Marchiney, E., Matchell, T., Mohabbat, K., Morgan, M., Morse, M., Moser, M., Neal, G., Marting, B., Martinde, B., Marting, B
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Submitted (24-SEP-2002) Human Genome Sequencing Center, Department
Emberollar and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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Submitted (27-58P-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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Contact: hgsc-help@bcm.tmc.edu
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Weinstock,G. and Gibbs,R.
Direct Submission
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Worley, K.C.
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REFERENCE AUTHORS TITLE JOURNAL

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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
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                             NOTE: This is a working draft' sequence. It currently consists of 26 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                   8: contig of 2358 bp in length
9: gap of unknown length
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0: contig of 2161 bp in length
0: gap of unknown length
0: contig of 2591 bp in length
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3: gap of unknown length
3: gap of unknown length
4: gap of unknown length
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128393: Gap of unknown length
138140: Contig of 9747 bp in length
138240: Gap of unknown length
158260: Contig of 12447 bp in length
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Matches 141; Conservative
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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oligo capping files
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Homo sapiens (human)
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Similarity 59.8%; Pred. No. 7.3e-05;
50; Conservative 0; Mismatches 95;
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NEDO human cDNA sequencing project
                                                                          'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                              /note="synonym: HIS1"
/db_xref="LocusID:3346"
/db_xref="MIM:142701"
Socation/Qualifiers
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Sugano, S. and Suzuki, Y.
Direct Submission
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gene="HTN1"
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268 TATAGAGGTTT 278
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I (bases 1 to 566)
Strausberg, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausberg, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marulana, R.F., Earmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Malek, J.A., Gararatae, P.H., Richards, S.W., Worley, K.C., Hale, S., Garcia, A.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Hellon, D.K., Maran, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Schley, M., Maden, A., Wong, A.C., Shevchenko, Y., Butterfield, Y.S., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marza, M.A.
WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Bmail: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: Aniord Diversity School of Medicine, Stanford, CA 94305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BC017835 566 bp mRNA linear PRI 04-OCT-2003 Homo sapiens histatin 1, mRNA (cDNA clone MGC:22502 IMAGE:4289874), complete cds.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21359663.
                                                                                                                 61 GGATITCAAGGTATITAAACACAGCAGTTTTCTAGCAAAGAACATCTCCTGAAGGATCAG 120
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Direct Submission
Submitted (03-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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BC017835.1 GI:17389614
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Homo sapiens
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Location/Qualifiers
1. .357
/organism='Unidentified'
                           Topology: Linear;
Secreted expressed sequence tags (sESTs)
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Pred. No. 0.00016;
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/note="unnamed protein product"
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/db_xref="GI:27899823"
/db_xref="REMTREMBL:CAD61372"
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/db_xref="taxon:9606"
                                                                                                                                                                                                  1. .357
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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/organism="Homo sapiens"
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al Similarity 59.4%;
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NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.
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F 10-APR-1997 US 08/838821

I KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI

DAVID MERBERG,
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Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
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TITLE Scretch expressed sequence tags (SESTS)
TOURNAL Patent: JP 2001519667-A 485 23-OCT-2001;
FM JP 2001519667-A 485
FM JP 2001519667-A/485
PR 10-APP 
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C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC Strandedness:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA
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12.7%; Score 77; DB 9; Length 323
Best Local Similarity 59.8%; Pred. No. 5.5e-05;
Matches 150; Conservative 0; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="salivary gland"
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Lplpeessksnanekhynllytlcfrilafsivt"
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                                                                                                                                   120 GAATTICATCITICATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTTCAT 179
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Full-length human cdnas encoding potentially secreted proteins
Patent: WO 02083898-A 22 24-OCT-2002;
                                                                 Gaps
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/note="Von Heijne matrix score 7.64030745849671 seq
ALVLALMISMISA/DS"
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Length 357;
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                                                                                                      120 GAATTTCATCTTTCATGACTGGACTCCAAATATGAAGATCTTTATCTTTGTCTTTCAT 179
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bejanin,S., Tanaka,H., Dumas Milne Edwards,J.B., Jobert,S. and Giordano,J.Y.
Full-length human cdnas encoding potentially secreted proteins
Patent: WO 02083898-A 358 24-OCT-2002;
GENSET (FR)
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A/Dote="VON Heijne matrix score 7.5999990463257
A/VALAMSMISA/DS"
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                                  Query Match 11.7%; Score 70.4; DB 6; Length 438; Best Local Similarity 69.9%; Pred. No. 0.0013; Matches 95; Conservative 0; Mismatches 41; Indels
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Sequence 358 from Patent WO02083898.
AX588483
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AX588483
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RESULT 7 AX616321

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84. 320
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       PAT 20-FEB-2003
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1 (bases 1 to 534)
Sabathini,L.M. and Azen,E.A.
Histatins, a family of salivary histidine-rich proteins, are encoded by at least two loci (HIS1 and HIS2)
Biochem. Biophys. Res. Commun. 160 (2), 495-502 (1989)
                                                                                                                                                                        Craniata, Vertebrata, Euteleostomi;
Catarrhini, Hominidae, Homo.
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Location/Qualifiers
1. .524
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                                                                                                                                                                                                                                                  Bejanin,S. and Tanaka,H.
Human odinas and proceins and uses thereof
Patent: WO 02094864-A 5 28-NOV-2002;
GENSET (FR)
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                                                                                                                          Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                         AX616321.1 GI:28447365
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polyA_site
ORIGIN
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SNYIVVDN
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                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRL Plate: 19 Row: o Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557652.

Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                            http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanle Rodrigues, Amy Sanchez and Michelle Whiting
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                        Contact: Gapbs-reamil.mih.gov
Inssue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
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Homo sapiens cDNA FLJ26103 fis, clone SLV07780.
AK129614
                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Butchow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wans, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavanch, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morernson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Rodrigues, S.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sanilus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marza, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                     /protein_id="AAA58646.1"
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/translation="MKFFVFALILALMLSMTGADSHAKRHHGYKRKFHEKHHSHRGYR
SNYLYDN"
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Homo sapiens histatin 3, mRNA (cDNA clone MGC:13578 IMAGE:4293405),
complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 558)
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Submitted (02-JUL-2001) National Institutes of Health, Mammalian
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 68.2; DB 9; Length 524;
Pred. No. 0.0034;
0; Mismatches 53; Indels
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             /db_xref="taxon:9606"
/tissue_type="parotid gland"
                                                                                                                                                                    /codon_start=1
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                                                                                       gene="HIS2"
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Matches 100; Conservative
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AUTHORS TITLE JOURNAL

COMMENT

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Sugano, S. and Suzuki, Y.

Sugano, S. and Suzuki, Y.

Direct Submission.

Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science, Submitted (31-JUL-2003) Sumio Sugano, S. and Submitted (31-JUL-2003) Sumio Submitted (31-JUL-2003) Sumio Submitted (31-JUL-2003) Sumio Submitted (31-JUL-2003) Sumio Submitted (31-JUL-2003) Submitted (
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NEDO human cDNA sequencing project supported by Ministry of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2073 CTIGGCTCTCATGCTTTCCATGACTGGAGCTGATTCACATGCAAAGAGACATCATGGGTA 2132
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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tissue [type="salivary gland"
|clone lib="SLV"
|note="cloning vector: pME185FL3"
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65.4%; Pred. No. 0.0027;
rative 0; Mismatches 53;
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oligo capping; fis (full insert sequence)
Homo sapiens (human)
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NEDO human cDNA sequencing project Unpublished
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/organism="Homo sapiens"
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Sugano, S. and Suzuki, Y.
Direct Submission
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Sugano, S. and Suzuki, Y.

Direct Submission

Direct Submission

Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,

Fax:81-3-5449-5416)

NEDO human cDNA sequencing project supported by Ministry of Fax:81-3-5449-5416

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Dapan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB; clone selection for full insert sequencing: RAB; clone selection for Location/Qualifiers
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Homo sapiens CDNA FLJ26993 fis, clone SLV03847, highly similar to alscatin 3 precursor.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                   Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., Hiraoka, S., Tanai, H., Watanabe, S., Ishida, S., Ono, Y., Botuta, T., Watanabe, M., Suzuki, Y., Hate, H., Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T., Izie, R., Oteuki, T., Sato, H., Nishikawa, T., Sugiyama, Y., Kawakami, B., Nagai, K., Isogai, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AK130503 AK130503.1 GI:34527320 oligo capping; fis (full insert sequence) Homo sapiens (human)
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NEDO human cDNA sequencing project
Unpublished
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nes 100; Conserv
                                                                                                                                                                                                                                                                                                                          Unpublished
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Query Match

ORIGIN

FEATURES

Best Loca Matches

d ŏ q ò AK130503 LOCUS DEFINITION

RESULT 11

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

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Gaps

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Length 2499;

179

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/protein_id="AAA60584.1"
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EQPLYPQPYQPYQQYTF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRI 13-JAN-1995
                                                                                                                                                                                                                                                                          140 GGACTCCACCAAATAIGAAGAICTITAICIITGTCTICAITAIGGCTCTCAGACTCCTAGCCA 199
                                                                                                                                                                                                                                                                                                Draft entry and computer-readable sequence [1] kindly submitted by L.Sabatini 19-JAN-1988.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                      260 GATA-----TITICAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 AATACCAACAATATACCTTTTAATATCATCAGTAACTGCAGGACATGATTATTGAGGCTT 282
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1 (bases 1 to 552)
Sabatini,L.M., Carlock,L.R., Johnson,G.W. and Azen,E.A.
CoDA cloning and chromosomal localization (4q11-13) of a gene for statherin, a regulator of calcium in saliva
Am. J. Hum. Genet. 41 (6), 1048-1060 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 CGT---ATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATTAGAGAGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Original source text: Human parotid gland, cDNA to mENA, clone H772B.
Draft entry and computer-readable secuence [1] kindly submitted
                                                                                                                                                                                                                                6
                                                                                                                                                                                     Length 542;
                                                                                                                                                                                   Score 67.6; DB 9; Length 5 Pred. No. 0.0044; 0; Mismatches 84; Indels
                                                                                                                          /product="statherin" 262 bp upstream of Pstl site; chromosome 4q11-q13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="STATH"
  /note="statherin signal peptide"
upstream of PstI site; chromosome 4q11-q13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                          57. .113
/gene="STATH"
/note="statherin signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      552 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulatory protein; statherin.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
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57. .113
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                                                                                                                                                                                       Query Match
Best Local Similarity 61.2%;
Matches 147; Conservative
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M18078.1 GI:338507
                                                                                       114. .242
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                          sig_peptide
                                                                                     mat_peptide
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HUMSTATHA
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VERSION
KEYWORDS
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TITLE
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Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction and 5'-end one pass sequencing: Institute of Medical
Science, University of Tokyo, Laboratory of Genome Structure, Human
Genome Center; 3'-end one pass sequencing: RAB; clone selection for
full insert sequencing: RAB and Helix Research Institute.

1. 2537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dickinson, D.P., Fidall, A.L. and Levine, M.J.
Human submandibular gland statherin and basic histidine-rich
peptide are encoded by highly abundant mRNA's derived from a common
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 CTTGGCTCTCATGCTTTCCATGACTGAGCTGATTCACATGCAAAGAGACATCATGGGTA 2170
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1 (bases 1 to 542)
Dickinson, D. P., Ridall, A.L. and Levine, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Original source text: Human female submandibuar gland, cDNA to mRNA, clone pBRHSNSF9B8.2.
Draft entry and computer readable copy of sequence [1] kindly provided by D.P.Dickinson 21-MAR-1988.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            120 GAATTTCATCTTTCATGACTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAAACGTCACAGGAA
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88106506
                                                                                                                                                                                                                                                                                                                                                                                                  53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                  tissue type="salivary gland"
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                                                                                                                                                                                                                                                                                                                                                           11.3%; Score 68.2; DB 9; 65.4%; Pred. No. 0.0026;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
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/gene="STATH"
/note="statherin precurser"
                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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Human statherin mRNA, complete cds.
                                                                                                                                                                     /organism="Homo sapiens"
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/db_xref="taxon:9606"
/map="4q11-q13"
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57. .245
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                   Local
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HUMSTTRNA
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AUTHORS
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1143 TGATTGGAGCTGATTCATCTGAAGAGAAATTTTTGCGTAGAATTGGAAGATTCGGTTATG 1202
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                                                                                        199
                                                                                                                                                                                                119 IGATTGGAGCTGATTCATCTCTGAAGAAATTTTGCGTAGAATTGGAAGATTCGGTTATG 178
                                                                                                                                                                                                                                                                                                    59 GAACCCAGCCAACTATGAAGTTCCTTGTCTTTGCCTTCATCTTGGCTCTCATGGTTTCCA 118
                                                                                                                                                                      260 GATA-----TITICAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTG 313
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                        140 GGACTCCACCAAATATGAAGATCTTTATCTTTTGTCTTCATTATGGCTCTCATCCTAGGCA
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                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Full-Length cDNA sequences Pull-Length cDNA sequences Patent: EP 1308459-A 1193 07-XAY-2003; Helix Research Institute (JP); Research Association for Biotechnology (JP)
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11.2%; Score 67.6; DB 6; Length 1584;
Best Local Similarity 61.2%; Pred. No. 0.0037;
Matches 147; Conservative 0; Mismatches 84; Indels 9;
Query Match 11.2%; Score 67.6; DB 9; Length 552; Best Local Similarity 61.2%; Préd. No. 0.0044; Matches 147; Conservative 0; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AX747668 1584 bp mRNA Sequence 1193 from Patent EP1308459. AX747668 1 GI:32132056
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Abx11391 Bovine hi	Abx11388 Bovine hi	Abx11389 Bovine hi	Abx11393 Bovine hi	Abx11394 Bovine ma	Abx11390 Bovine hi	-	EST Cl	Human	Abz36590 Human GEN	Abz36425 Human GEN	Aah98658 Human EST	Aaa48964 Human sta	Ade40261 Human NOV	Adb63039 Human cDN	Aav89600 EST clone	Aaa48965 Human bas		Ade07409 Novel cod	Aav89525 EST clone	Aal60905 Human sal	Aal61238 Human sec	Abq99552 Human cod
ΙD	ABX11391	ABX11388	ABX11389	ABX11393	ABX11394	ABX11390	ABX11392	AAV89526	ACC51062	ABZ36590	ABZ36425	AAH98658	AAA48964	ADE40261	ADB63039	AAV89600	AAA48965	ADE09636	ADE07409	AAV89525	AAL60905	AAL61238	ABQ99552
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* Query Match	100.0	77.1	74.2	70.1	39.5	19.0	14.4	12.5	11.7	11.7	11.7	11.3	11.2	11.2	11.2	11.1	10.4	10.3	10.1	10.1	10.1	6.6	9.6
Score	604	465.4	448.2	423.4	238.4	115	87	75.4	70.4	70.4	70.4	68.2	67.6	67.6	67.6	67.2	62.6	62	60.8	60.8	60.8	59.6	28
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Aav89602 EST clone		Abl32961 Human imm	Ab132298 Human imm	Aas46659 Tumour su	Abl33478 Human imm	Abl32084 Human imm	σ.	a	Ada71938 Rice gene	'n	Ab192319 Chemicall	Abl32777 Human imm		Abk31238 Signal tr	Ada20354 Prostate	Ada84161 Human ren	Adb54121 Pretreate	Adb54249 Pretreate	Abl32766 Human imm	Abk28362 DNA trans	Ab192265 Chemicall
2 AAV89602	6 ABL33385	6 ABL32961	6 ABL32298	4 AAS46659	6 ABL33478	6 ABL32084	6 ABL32989		7 ADA71938	6 ABL34125		6 ABL32777	4 AAS46321		7 ADA20354	7 ADA84161	9 ADB54121	9 ADB54249		6 ABK28362	6 ABL92265
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55.8	53.6	51.2	51	51	49.8	49.4	49.4	49.2	49	49			47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.2	47.2
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ALIGNMENTS

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New histatin polynucleotides and polypeptides expressed in bovine tissues, useful for treating bacterial or fungal infections in mammals, e.g. infections of the oral cavity, vagina, urethra, ear or skin, or systemic infections.
                                                                                                                    Cow; gene; ss; histatin; bovine; salivary secretion; oral cavity; non-immune defence system; oral candidosis; gene therapy; microbial infection; fungal infection; dental caries; plaque; tartar; cystic fibrosis; systemic infection; Candida infection; mastitis; fungicide; antibacterial:
                                                                                                                                                                                                                              Location/Qualifiers
154. 330
/*tag= a "Histatin like polypeptide"
/product= "Histatin like polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molenaar AJ, Davis SR;
                                                                                                  Bovine histatin like polypeptide, #4, cDNA.
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                      BP.
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29-OCT-1999; 99US-0162701P.
22-AUG-2000; 2000US-00644190.
27-OCT-2000; 2000US-00699146.
                                                                                                                                                                                                                                                                                                                                                     19-FEB-2002; 2002US-00079754.
                       ABX11391 standard; cDNA; 604
                                                                          (first entry)
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                                                ABX11391;
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RESULT 1
             ABX11391
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ABX11388 standard; cDNA; 505

RESULT 2

ABX11388

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conjugated the proposes isociated niversed in bovine. Histatins are histidine rich and specific to the salivary secretions. They are believed to the function as part of the non-immune defence system, particularly in the carl cavity and have promise as therapeutic agents in humans with oral cavity and have promise as therapeutic agents in humans with oral carl cavity and have promise as therapeutic agents in humans with oral candidesis. Also disclosed are compositions comprising the histatin of polyapetide, and at least one component consisting of physiological or pharmaceutical carriers or immunostimulants. The histatin polynucleotide, polyapetide, or the cosmetic composition comprising the polyapetide, is useful for treating (e.g. gene therapy) a discrete in a mammal, particularly microbial or fungal infections. The histatin polynucleotide is also useful in genome mapping, physical captured or polymosical is also useful for treating fungal or bacterial infections of the oral cavity (e.g. dental caries, plaque or tartar), vagina, urethra, ear, skin, respiratory tract (e.g. cystic fibrosis caused by Pseudomonas aerudinosal, mucosa or eye, as well as for treating systemic infections such as systemic Candida infection. The polyapetide or polymosities is also useful for veterinary applications e.g. for treating mastitis. The sequence presented is a cDNA encoding a bovine the infection in the polypeptide.
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                                invention discloses isolated histatin
Claim 1; Page 12; 17pp; English
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The invention discloses isolated histatin polymucleotides and polymeptides, which comprise sequences expressed in bovine. Histatins are histatine rich and specific to the salivary secretions. They are believed to function as part of the non-immune defence system, particularly in the cardidosis. Also disclosed are compositions comprising the histatin polymeptide or polymelectide, and at least one compositions with oral caption of pharmaceutical carriers or immunostimulants. The histatin polymelectide, polymeptide, for the comment consisting of histatin polymelectide, polymeptide or perfect or composition or in the polymeptide, is useful for treating (e.g. gene therapy) a disorder in a mammal, particularly microbial or fungal infections. The histatin polymelectide is also useful in genes Specifically, the polymeptide or polymelectide is useful for treating fungal or bacterial infections of the oral cavity (e.g. deneal caries, plaque or tartar), caused by Pseudomonas aeruginosa), mucosa or eye, as well as for treating caused by Pseudomonas aeruginosa), mucosa or eye, as well as for treating entering and manning or the cardidate in urethra, ear, skin, respiratory tract (e.g. cystic fibrosis or systemic infections such as systemic candidations. The polymeptide or polymeric contract or eye, as well as for treating experiment infections such as systemic candidations. The polymeptide or polymeric candidations. The polymeric plants of the cardidations or eye, as well as for treating experiment infections such as systemic candidations. The polymeric plants or the cardinations of the cardidations or eye, as well as for treating experiment infections such as systemic cardidations. The polymeric plants are polymericant or plants are proposed and plants are plants are plants.
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                                                                                                                                                               Cow, gene, ss, histatin, bovine, salivary secretion, oral cavity;
non-immune defence system, oral candidosis, gene therapy,
microbial infection, fungal infection, dental caries, plaque; tartar;
cystic fibrosis, systemic infection, Candida infection, mastitis;
                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a /*tag= a //product= "Histatin like polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SR;
                                                                                                                    Bovine histatin like polypeptide, #1, cDNA
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44. .220
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29-0CT-1999; 99US-0162701P.
22-AUG-2000; 2000US-00644190.
27-OCT-2000; 2000US-0069146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-FEB-2002; 2002US-00079754
                                                                       (first entry)
                                                                                                                                                                                                                                                                fungicide; antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glenn M, Grigor MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       systemic infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; ABG75791.
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                                                                       01-MAY-2003
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                                                                                                                                                                                                                                                                                                                  Bos taurus.
                         ABX11388;
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Sequence 505 BP; 188 A; 96 C; 67 G; 154 T; 0 U; 0 Other;

us-10-079-754a-4.rng

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                                                                                                   88 CATGATTAGAGCTGATTCATCTGAAGAGAAAACGTCACAGGAAACGGAAAAAAACATCATAG
                                                                                                                                                                                           328 AAAAAAATCAGTCAAGTAGTIGCACAACACATACTIGGAATCAAATATCAATATTTAA
                                                                                     148 AGGATATTTTCAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTA
                                                                                                                                                                          TCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATTAGAGAGATTTTCACAA
                                                                                                                                                                                                                     TGATTTTTCCTACTCTTTCTGTTGTGTTGAAAACCATCTTTCAAATGAATAAAACAAAGA
                                                                                                                                                                                                                                                                 AAAAAAATCAGTCAAGTAGTTGCACACACATACTTGGAATCAAATATCAATATTTTAA
                                                                                                                                                                                                                                                                                                           Cow; gene; ss; histatin; bovine; salivary secretion; oral cavity; non-immune defence system; oral candidosis; gene therapy; microbial infection; fungal infection; dental caries; plaque; tartar; cystic fibrosis; systemic infection; Candida infection; mastitis;
                                            138 CTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCAGC
                                                          AGGATATTTTCAACAATACCAGCCATATCAAGGATATCCACTAAATTATCCTGCGTA
                       Gaps
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0
   Length 505;
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= "Histatin like polypeptide"
  7;
  Score 465.4; DB 7
Pred. No. 2.4e-90;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovine histatin like polypeptide, #2, cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
149. .325
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29-0CT-1999; 99US-0162701P.
22-AUG-2000; 2000US-00644190.
27-OCT-2000; 2000US-00699146.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ABX11389 standard; cDNA; 585
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   77.1%;
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Query Match
Best Local Similarity 99.8
Matches 466; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fungicide; antibacterial
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the invention unsergoes sequences expressed in border. Histatins are instituted, which comprise sequences expressed in border. Histatins are histidine rich and specific to the salivary secretions. They are believed to function as part of the non-immune defence system, particularly in the cord cardity and have promise as therapeutic agents in humans with oral cardity and have promise as therapeutic agents in humans with oral candidosis. Also disclosed are compositions comprising the histatin of polypeptide or polymenticedide, and at least one component consisting of physicological or pharmaceutical carriers or immunostimulants. The histatin polymucleotide, polypeptide, or the cosmetic composition of discret in a mammal, particularly microbial or fungal infections. The histatin polymucleotide is also useful for treating (e.g. gene therapy) a cincatin polymucleotide is also useful for treating fungal or bacterial colling of genes. Specifically, the comprision of the oral cavity (e.g. dental caries, plaque or tartar), cappactions of the oral cavity (e.g. dental caries, plaque or tartar), cappactions such as systemic Candida infections are polypeptide or polymucleotide is useful for treating as well as for treating systemic infections such as systemic Candida infection. The polypeptide or polymucleotide is also useful for veterinary applications e.g. for treating mastitis. The sequence presented is a cDNA encoding a bovine content in the polypeptide or polymorphyse presented is a cDNA encoding a bovine content of the content of th
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                                                                                                                       New histatin polynucleotides and polypeptides expressed in bovine tissues, useful for treating bacterial or fungal infections in mammals, e.g. infections of the oral cavity, vagina, urethra, ear or skin, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 caggacrocaccaaarargaagarcrirarcrirarcrirargecrocaccaraccage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATTAGAGAGATTTTTCACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
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99.3%; Pred. No. 1.2e-86;
tive 0; Mismatches 3;
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                Davis SR;
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                   Molenaar AJ,
                                                                                                                                                                                                                                           Claim 1; Page 11; 17pp; English
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Best Local Similarity 99.3
Matches 450; Conservative
                   Grigor MR,
                                                                                                                                                                                             systemic infections.
                                                              WPI; 2003-275306/27
                                                                                   P-PSDB; ABG75792
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                   Glenn M,
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Length 525;

ABX11393 RESULT

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al Similarity 93.4%;
466; Conservative
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Query Match
Best Local 9
                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New histatin polynucleotides and polypeptides expressed in bovine tissues, useful for treating bacterial or fungal infections in mammals, e.g. infections of the oral cavity, vagina, urethra, ear or skin, or systemic infections.
                                                                                                                                                                                                                                                                          Cow, gene, ss, histatin, bovine, salivary secretion, oral cavity; non-immune defence system; oral candidosis, gene therapy, microbial infection, fungal infection, dental caries, plaque; tartar, cystic fibrosis, systemic infection, Candida infection, mastitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "Histatin like polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Davis SR;
                                                                                                                                                                                                                                Bovine histatin like polypeptide, #6, cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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2000US-00644190.
                                                                             ABX11393 standard; cDNA; 525
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                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     fungicide, antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glenn M, Grigor MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-275306/27
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22-AUG-2000;
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                                                                                                                                                                             01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus
                                                                                                                                ABX11393,
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C; 72 G; 164 T; 0 U; 0 Other;

Sequence 525 BP; 187 A; 102

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255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cow; ss; histatin; bovine; salivary secretion; oral cavity; non-immune defence system; oral candidosis; gene therapy; microbial infection; fungal infection; dental caries; plaque; tartar; cystic fibrosis; systemic infection; Candida infection; mastitis; fungicide; antibacterial; mammary-gland.
                                                                                                                                                             CATGATTAGAGCTGATTCATCTGAAGAAAACGTCACAGGAAAAGGAAAAAACATCATGT
                                                                                                                                                                                                                                                                                                                                                                                                              CACATACTTGGAATCAAATATCAATATTTTAAAACATAATAATGATAGTGCTCTGGAACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 caggacticcaccaatatgaagatctttatctttgtcttcattatggctctcatcctagc
                                                                                                                                         CATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAAACGGAAAAAAACATCAT--
                                                                                                                                                                                                                                147 IGATAGGICTCCAGAATICTTACTAATACAAGAGATATTTTTCAACAATACCAGCCATAT
                                                                                                                                                                                                                                                                   CAACGATATCCACTAAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAA
                                                                                                                                                                                                                                                                                                  caacgararccacraaarrarccrccrccrarccarrrccrraaaargcrccrraaa
                                                                                                                                                                                                                                                                                                                                                              cracaggacargarragagagarrrrrcacaargarrrrrccracrcrrrrcrgrrgrr
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACATACTTGGAATCAATATTTTAAAACATAATAATGATGGTAGTCTCTGAACTAT
                                                                                                                                                                                                     -----AGAGGATATTTTCAACAATACCAGCCATAT
                                                                                                                                                                                                                                                                                                                                CTACAGGACATGATTAGAGAGATTTTTCACAATGATTTTTCCTACTCTTTCTGTTGTTT
                                                 Gaps
                                              32;
                                                Indels
Score 423.4; Db ,,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Davis SR;
                               Pred. No. 2.46
0; Mismatches
                                                                               CIGGACICCACCAAATAIGAAGAICITIAICII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glenn M, Grigor MR, Molenaar AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine mammary tissue cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCAAGCATAAAAAAAAA 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    507 ATCAAGCATAAAAAAAA 525
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29-0CT-1999; 99US-0162701P.
22-AUG-2000; 2000US-00649190.
27-OCT-2000; 2000US-00699146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-FEB-2002; 2002US-00079754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABX11394 standard; cDNA; 267
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The invention discloses isolated histatin polynuclectides and polypeptides, which comprise sequences expressed in bovine. Histatins are polypeptides, which comprise sequences expressed in bovine. Histatins are histatine rich and specific to the salivary secretions. They are believed to function as part of the non-immune defence system, particularly in the candidosis. Also disclosed are compositions comprising the histatin of polypeptide or polynuclectide, and at least one component consisting of physiological or pharmaceutical carriers or immunosimulants. The comprising the polypeptide, particularly microbial or fungal infections. The discret in a mammal, particularly microbial or fungal infections. The comprising the polypeptide, is useful for treating (e.g. gene therapy) a discret in a mammal, particularly microbial or fungal infections. The polypeptide is also useful in genome mapping, physical mapping or in the positional cloning of genes. Specifically, the confidence or polymuclectide is also useful for treating fungal or bacterial infections of the oral cavity (e.g. dental caries, plaque or tartar), vagina, urethra, ear, skin, respiratory tract (e.g. cystic fibrosis caused by Resudomonas aeruginosa), mucosa or eye, as well as for treating systemic infections such as systemic Candida infection. The polypeptide or prolymuclectide is also useful for veterinary applications e.g. for creating mastitis. The sequence presented is the bovine mammary tissue or companies.
                                                                            New histatin polynucleotides and polypeptides expressed in bovine tissues, useful for treating bacterial or fungal infections in mammals, e.g. infections of the oral cavity, vagina, urethra, ear or skin, or
                                                                                                                                                                                                                         Example 2; Page 15; 17pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -gland specific sequences
                                                                                                                                         e.g. infections of t
systemic infections.
                           WPI; 2003-275306/27
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Sequence 267 BP; 89 A; 59 C; 43 G; 76 T; 0 U; 0 Other;

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                                                                         197
                                                                                                                                               257
                                                                                                                                                                                                                                        148 AGGATATTTTCAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTA 207
                                                                                                                                                                                                                                                                                                              TCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATTAGAGAGATTTTTCACAA 267
                                                                                                                                                                                 AGGATATTTTCAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTA 317
                                                                                                                                                                                                                                                                                         TCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATTAGAGAGATTTTCACAA 377
                                                                                                           87
                                                                         CTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGC
                                                                                                             CAGGACTCCACAAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGC
                                                                                                                                                 CATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAAACGGAAAAAACATCATAG
                                     Gaps
                                   0;
 DB 7; Length 267;
                                     Indels
Query Match 39.5%; Score 238.4; DB 7; Best Local Similarity 99.6%; Pred. No. 8.9e-42; Matches 239; Conservative 0; Mismatches 1;
                                                                         138
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Cow, gene, ss, histatin, bovine, salivary secretion, oral cavity, non-immune defence system, oral candidosis, gene therapy; microbial infection; fungal infection; dental caries; plaque; tartar; cystic fibrosis; systemic infection; Candida infection; mastitis; fungicide; antibacterial.
                                                                                                                  Bovine histatin like polypeptide, #3, cDNA.
                             ВP
                             ABX11390 standard; cDNA; 869
                                                                                       (first entry)
                                                                                         01-MAY-2003
                                                           ABX11390;
RESULT 6
ABX11390
                             SXEXEXEXAXO
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ATGTATTCCTC

176

RESULT

taurus

Bos

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polypeptides, which comprise sequences expressed in bowine. Histatins are histidine rich and specific to the salivary secretions. They are believed to function as part of the non-immune defence system, particularly in the coral cavity and have promise as therapeutic agents in humans with oral cavity and have promise as therapeutic agents in humans with oral cavity and have promise as therapeutic agents in humans with oral candidosis. Also disclosed are compositions comprising the histatin of polypeptide or polymentoeride, and at least one component consisting of physiological or plarmaceutical carriers or immunostimulants. The comprising the polypeptide, particularly microbial or fungal infections. The histatin polymucleotide is useful for treating (e.g. gene therapy) a discorder in a mammal, particularly microbial or fungal infections. The histatin polymucleotide is also useful for treating fungal or bacterial corplypeptide or polymucleotide is useful for treating fungal or bacterial corplinations of genes. Specifically, the confinence or polymucleotide is useful for treating fungal or bacterial caused by Resudomonas acruginosa), mucosa or eye, as well as for treating systemic infections such as systemic Candida infection. The polympetide or prolymucleotide is also useful for veterinary applications e.g. for treating mastitis. The sequence presented is a cDNA encoding a bovine construction like polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New histatin polynucleotides and polypeptides expressed in bovine tissues, useful for treating bacterial or fungal infections in mammals, e.g. infections of the oral cavity, vagina, urethra, ear or skin, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 115; DB 7; Length 869;
Pred. No. 2.9e-15;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 869 BP; 282 A; 157 C; 147 G; 283 T; 0 U; 0 Other;
                                                       /*tag= a
/product= "Histatin like polypeptide'
                                                                                                                                                                                                                                                                                                                                                                              Molenaar AJ, Davis SR;
                 Location/Qualifiers 72. .284
                                                                                                                                                                                                                                                                                                                                        (GENE-) GENESIS RES & DEV CORP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 12; 17pp; English
                                                                                                                                                                                                                                                    29-OCT-1999; 99US-0162701P.
22-AUG-2000; 2000US-00644190.
27-OCT-2000; 2000US-00699146.
                                                                                                                                                                                               19-FEB-2002; 2002US-00079754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 92.4%;
Matches 121; Conservative (
                                                                                                                                                                                                                                      99US-0150330P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 AGGATATTTTC 268
                                                                                                                                                                                                                                                                                                                                                                              Glenn M, Grigor MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           systemic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-275306/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; ABG75793.
                                                                                                                   US2002164625-A1.
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                                                                                                                                                         07-NOV-2002
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Length 96;

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The invention discloses isolated histatin polynucleotides and colypeptides, which comprise sequences expressed in bovine. Histatins are polypeptides, which comprise sequences expressed in bovine. Histatins are histation as part of the non-immune defence system, particularly in the coral cavity and have promise as therapeutic agents in humans with oral cavity and have promise as therapeutic agents in humans with oral cardidosis. Also disclosed are compositions comprising the histatin oplymorpectice, and at least one component consisting of physiological or pharmaceutical carriers or immunostimulants. The comprising the polypeptide, is useful for treating (e.g. gene therapy) a discrder in a mammal, particularly microbial or fungal infections. The nistatin polymucleotide is also useful in genome mapping, physical caused the oral cavity (e.g. dental caries, plaque or tartar), the polypeptide or polymucleotide is useful for treating fungal or bacterial infections of the oral cavity (e.g. dental caries, plaque or tartar), vagina, urethra, ear, skin, respiratory tract (e.g. cystic fibrosis caused by Pseudomonas aeruginosa), mucosa or eye, as well as for treating systemic infections such as systemic Candida infections. The sequence presented is a convertion a bovine treating mastitis. The sequence presented is a convertion as bovine pretatin like polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New histatin polynucleotides and polypeptides expressed in bovine tissues, useful for treating bacterial or fungal infections in mammals, e.g. infections of the oral cavity, vagina, urethra, ear or skin, or systemic infections.
                                                                                                                                    Cow; gene; ss; histatin; bovine; salivary secretion; oral cavity; mon-immune defence system; oral candidosis; gene therapy; microbial infection; fungal infection; dental caries; plaque; tartar; cystic fibrosis; systemic infection; Candida infection; mastitis; fungicide; antibacterial.
                                                                                                                                                                                                                                                                                                                                             *tag= a /*tag= histatin like polypeptide" /pratiduc //partiduc //partiduc //hote= "No start or stop codon shown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Davis SR;
                                                                                                             Bovine histatin like polypeptide, #5, cDNA.
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molenaar AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 12; 17pp; English.
ABX11392 standard; cDNA; 96 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-AUG-1999; 99US-0150330P.
29-0CT-1999; 99US-0162701P.
22-AUG-2000; 2000US-00699146.
27-OCT-2000; 2000US-00699146.
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                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-275306/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             US2002164625-A1.
                                                                           01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-2002
                                                                                                                                                                                                                                                                    Bos taurus
                                    ABX11392;
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Sequence 96 BP; 33 A; 25 C; 10 G; 28 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 GACTCTCTCTTGAGAAGGACTCAGCCAACTATGAAGTTTTTTGTCTTTAGT 107
                                                                                                                                                                                                                                                                                                                                                                                     Human; secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EST). The
                                                                324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliocating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, hematopolesis regulating activity, issue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemacotatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for
                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from e.g.
                                                                                             1 Tricaacaataccaaccaratgaaccararccacraaarrarccrccrccracra
                                                            265 ITTCAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTGCGTATCCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides encoding human secreted proteins - derived fr
human blood, kidney, foetal lung, placenta, testes, brain, ovary,
pituitary, retina and colon cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 357 BP; 101 A; 74 C; 65 G; 117 T; 0 U; 0 Other;
                              5; Indels
                                                                                                                                  325 CCTTAAAATGCTGCTTAGTAACTACAGGACATGAT 359
                                                                                                                                                                 S
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Racie LA,
Score 87; DB 7;
Pred. No. 2e-09;
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                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 245; 618pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US006955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-00838821.
   14.4%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 59.4%;
Matches 149; Conservative
                                                                                                                                                                                                                                                         AAV89526 standard; cDNA; 357
                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GEMY ) GENETICS INST INC.
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-070077/06.
Query Match
Best Local Similarity
Matches 90; Conserv
                                                                                                                                                                                                                                                                                                                                                             EST clone CP294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9845436-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-APR-1997;
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                                                                                                                                                                                                                                                                                           AAV89526;
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8 g ઠે

110 crrescrictcargartrecardarrascecricarreacardaaaaagacarcargsgra 169

240 ACGGAAAAAACATCAT 255

180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA

239

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167
                                                               299
                                                                                                                                                               281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel human GENSET coding sequences ACC51060-ACC51115) and proteins (ABR46453-ABR48508). The GENSET sequences are useful for preparing a composition for treating GENSET related disorders. They can also be used as markers for tissues in which the corresponding protein is preferentially expressed, as molecular weight markers on Southern gels, as chiromosome markers or tags to identify chromosomes, and as reagents in assays to quantitatively
                                                               240 ACGGAAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT
                               CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAAGAGACATCATGGGTA
                                                                                                                               300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT
                                                                                                                                                               222 GGACTGTGGATCAATTATCTATATGACAATTGATATCCTTAGTAATCATGGGGCATGAT
TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA
                                                                                             168 Tagaagaaantccar----gaaaagcarcaricacarcgagaartrccarrintargg
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in
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69.9%; Pred. No. 9.3e-06;
cive 0; Mismatches 41; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; GENSET; therapeutic; therapy; gene; ss
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                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                  Human Chimerin coding sequence.
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15-UUN-2001; 2001US-0298698P.
29-UUN-2001; 2001US-0302277P.
13-UUL-2001; 2001US-0305456P.
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                                                                                                                                                                                                                                                                                                               ACC51062 standard; cDNA;
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The present invention relates to novel GENSET polynucleotides (ABZ36404-ABZ36911) encoding polypeptides (ABP75963-ABP76368). The polynucleotides and polypeptides are useful in screening and diagnostic assays for abnormal GENSET expression and/or biological activity. They are also useful for screening of compounds for treating or preventing GENSET-related disorders, such as heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity. The polynucleotides are useful for constructing or expanding chromosome maps
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                                                                                                                                                                                                                                                                                                                                                                                                     Human GENSET coding sequence SEQ ID 358.
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                                                                                                                                                                                 ABZ36590 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                      Dumas Milne Edwards J,
                                                                                                                                                               Human GENSET coding sequence SEQ ID 22.
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                                                                                       ABZ36425 standard; cDNA; 438 BP
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Matches 95,
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                                                                                                                                     Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.
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                                                                                                  Human EST-derived coding sequence SEQ ID NO: 515.
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Zhang J, Werhman T;
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17-JUL-2000; 2000US-00617746.
03-AUG-2000; 2000US-00631451.
15-SEP-2000; 2000US-00663870.
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AAA48964
ID AAA48964 standard; DNA; 552 |
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Cao Y, Drmanac RA,
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239 AATACCAACAATATACCTTTTAATATCATCAGTAACTGCAGGACATGATTATTGAGGCTT 298
                                                                              BP.
                                                                                                                                                                             Human NOV38a cDNA - SEQ ID 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001US-0314031P.
2001US-0314466P.
2001US-0315403P.
2001US-0315853P.
2001US-0322716P.
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2002US-0354591P.
                                                                              ADE40261 standard; cDNA; 678
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17-AUG-2001;
17-AUG-2001;
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20-AUG-2001;
21-AUG-2001;
23-AUG-2001;
28-AUG-2001;
29-AUG-2001;
17-SEP-2001;
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05-FEB-2002;
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07-JUN-2002;
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                                                                                                               ADE40261;
                                                 RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to human lysine-rich statherin protein (LRSP) (AAY94526). The cDNA sequence encoding this protein was identified through analysis of a cDNA library of breast tumour tissue (BRSTNOT14). The LRSP sequence was found to have homology with the DNA of human estatherin (the present sequence) and human basic histidine-rich protein (AAY94528). Human statherin is a phosphoprotein that acts as an inhibitor of precipitation of calcium phosphate salts in the oral cavity. The LRSP polypeptide and its antagonists may be useful for treating or preventing disorders associated with the activity of LRSP. Such disorders include dutoimmune/inflammatory disorders (for example AIDS, allergies, asthma, diabetes mellitus), bacterial and fungal infection and cancers (such as leukemia, adenocarcinoma, melanoma). Antibodies to LRSP may be useful for diagnosis of the above disorders
                                                                                            Lysine-rich statherin protein; LRSP; acidic phosphoprotein; human; precipitation inhibitor; autoimmune; inflammatory disorder; AIDS; asthma; allergy; diabetes mellitus; fungal; bacterial infection; cancer; leukemia; adenocarcinoma; melanoma; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTATATGGCTCTCATCCTAGCCA 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purified polypeptide used for treating or preventing a disorder characterized by expression or activity of lysine-rich statherin
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/product= "Statherin"
                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 71; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guegler KJ,
                                                                                                                                                                                                                                                                                                                                                        99WO-US024046
                                                                                                                                                                                                                                                                                                                                                                                       98US-0155209P
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Best Local Similarity 61.2%;
Matches 147; Conservative
                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corley NC,
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P-PSDB; AAY94527.
                                                               Human statherin DNA
                                                                                                                                                                                                                                                                                          WO200024779-A1
                                                                                                                                                                             Homo sapiens
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                                06-OCT-2000
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 AAA48964;
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cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
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                                                                                                         antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic; antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes; AlDS; multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's; asthma; fertility disorder; vaccine; gene therapy; chromosome mapping; tissue typing; human; NOV; ss; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK;
Shimkets RA, Zerhusen BD, Li L, Ji W, Padigaru M, Casman SJ;
Voss EZ, Boldog FL, Gorman L, Leite MW, Vernet CAM, Anderson DW;
Guo X, Zhong M, Gerlach VL, Hjalt T, Rastelli L, Spytek KA;
Edinger SR, Ellerman X, Malyankar UM, Macdougall JR, Stone DJ;
Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;
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Search completed: August 15, 2004, 21:45:07 Job time : 355 secs
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                                   The invention relates to a novel NOVX polypeptide. The polypeptide-of the invention demonstrates cardiant, antiarteriosclerotic, hypotensive, cytoscatic, ancrectic, antidiabetic, immunosuppressive, anti-HIV, neuroprotective, nootropic, antidiabetic, immunosuppressive, anti-HIV, neuroprotective, nootropic, antiparkinsonian, antidasthmatic and gynaecological activities and may be useful in diagnosing, treating or preventing NOVX-associated disorders including cardiomyopathy, preventing NOVX-associated disorders including cardiomyopathy, atherosciarosis, hypertension, cancer, obesity, diabetes, AIDS, multiple sclerosis, graft-versus-host disease, Alzheimer's disease, ABRA mantiple be utilised as vaccines whilst the nucleic acids may be used as hybridisation probes, in gene therapy, chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The current sequence is that of the human NOV CDNA of the invention.
                                                                                                                                                                                                                                                                                                                                              315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGACTCCACCAAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCGTAGCCA
                                                                                                                                                                                                                                                                                                                                               256 gaacccagccaacrargaagrrccrrgrcrrrgccrrcarcrrggcrcrcarggrrrcca
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                                                                                                                                                                                                                                                             6; DB 9; Length 678;
4e-05;
ches 84; Indels
                                                                                                                                                                                                                                 Sequence 678 BP; 190 A; 151 C; 137 G; 200 T; 0 U; 0 Other;
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89. .997
/*ttag = "Clone SALGL10001070 protein"
/product = "Clone SALGL10001070 protein"
                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                             / Match 11.2%; Score 67.6; Local Similarity 61.2%; Pred. No. 4e les 147; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cDNA encoding clone SALGL10001070
                 Claim 20; SEQ ID NO 167; 560pp; English.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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25-JAN-2002; 2002US-00350978.
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The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel conditions and also claimed is a polypeptide encoded by the polynucleotide. Or lits partial peptide, an antibody binding to the polypeptide or peptide or the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide or the polynucleotide by contacting the polypeptide or peptide or the antibody of the encoded protein and observing the binding between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide of a useful as a primer for synthesising the polynucleotide, or as a probe contact of a useful as pharmaceutical agents and many disease-related proteins are useful as pharmaceutical agents and many disease-related confidence for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell capencial transcription-related proteins, signal transduction-related proteins, concoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours: The colba may be used to regulate the activity or expression of the invention. Note: Some of the sequence contact of the activity or expression of the invention. Note: Some of the sequence of the activity or expression of the invention. Note: Some of the sequence of the
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Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                       New polynuclectides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.
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is based on sequence information supplied by the Buropean Patent Office.
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                           Sugiyama T,
                                                                      Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                          WPI; 2003-450961/43
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                                Isogai T,
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RESULT 2
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                                                                                                                     August 15, 2004, 21:39:53 ; Search time 73 Seconds (without alignments) 4591.648 Million cell updates/sec
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1: /cgn2 6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2 6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2 6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2 6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2 6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2 6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-702-705-214
US-09-702-705-214
US-09-614-1248-214
US-09-671-325-214
US-10-204-708-26
US-10-204-708-26
US-10-204-708-26
US-10-204-708-26
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US-10-204-708-39
US-09-468-66-4
US-09-023-655-197
US-09-037-895-29
US-08-981-803-29
US-08-981-803-29
US-08-993-460-29
US-08-973-462-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                    using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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No.
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28 39.2 6.5 832 4 US-09-621-976-2813 Sequence 2813, Ap 30.2 6.5 19124 2 US-09-61-976-2813 Sequence 2813, Ap 5.5 19124 2 US-08-916-2813 Sequence 13, App1 3 6.5 19124 2 US-08-916-4218-13 Sequence 13, App1 5 6.5 19124 2 US-08-916-4218-13 Sequence 13, App1 5 6.4 19124 2 US-08-916-918 Sequence 13, App1 5 6.3 38.4 6.4 989 3 US-08-917-926-2 Sequence 2706, Ap 5 8 6.3 10.467 4 US-09-514-618-2 Sequence 19, App1 5 6.3 10.467 4 US-10-24-19 Sequence 2, App1 6 6.3 10.467 4 US-10-24-19 Sequence 2, App1 6 6.3 10.467 4 US-10-24-19 Sequence 2, App1 6 6.3 10.467 4 US-10-20-19 Sequence 2, App1 6 6.3 10.467 4 US-10-20-19 Sequence 2, App1 6 6.2 5535 4 US-10-20-19 Sequence 2, App1 6 6.2 5535 4 US-10-20-19 Sequence 2, App1 6 6.2 5536 4 US-10-20-19 Sequence 2, App1 6 6.2 5536 4 US-10-20-18 Sequence 2, App1 6 6.2 5540 4 US-10-20-18 Sequence 2, App1 6 6.2 5550 4 US-10-20-18 Sequence 2, App1 6 6.2 5560 4 US-10-20-18 Sequence 6, App1 6 6.2 5560 4 US-10-20-18 Sequence 6, App1 6 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.40 6.3 10.4
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ALIGNMENTS

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518530 TATAAAAATTAGAAAAACAACTAAAATTAATGGTTTTAGAAAAGGAAAAACTCCTATTAG 518589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 GATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATC
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Sequence 1, Application US/09790988

Patent No. 6632935

GENERAL INFORMATION:

APPLICANT: SHIGENOBU, SHUUI

APPLICANT: HATTONE, MASAHIRA

APPLICANT: HATANABE, HIDEMI

APPLICANT: APPLICANT: GENOWE DNA OF BACTERIAL SYMBIONT OF APHIDS

FILE REPRENENCE: 081356/0159

CURRENT APPLICATION NUMBER: UP2000-107160

PRIOR PILING DATE: 2001-02-23

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 7
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7.0%; Score 42.4; DB 4; Length 6
Best Local Similarity 47.4%; Pred. No. 1.8;
Matches 127; Conservative 0; Mismatches 141; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CORGANISM: Buchnera sp.
US-09-790-988-1
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ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
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US-10-204-708-38/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306 TCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATTAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366 GATTTTTCACAATGATTTTTCCTACTCTTTCTGTTGAAAACCATCTTTCAAATGA
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                                                                                                                                                                  APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REPERENCE: 081356/0159
CURRENT APPLICATION UNMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-204-708-28/C
| JOS-10-204-708-28/C
| Patent No. 667731
| GENERAL INFORMATION |
| GENERAL INFORMATION |
| APPLICANT: DIEPENBROCK, Christian |
| APPLICANT: DEELIN, KURT |
| TITLE OF INVENTION: Diagnosis of Diseases Associated |
| TITLE OF INVENTION: Dy Assessing DNA Methylation |
| FILE REFERENCE: 5013.1012 |
| CURRENT APPLICATION NUMBER: US/10/204,708 |
| CURRENT APPLICATION NUMBER: DT/EP01/03971 |
| PRIOR FILING DATE: 2001-04-06 |
| PRIOR FILING DATE: 2000-04-06 |
| PRIOR FILING DATE: 2000-04-06 |
| PRIOR FILING DATE: 2000-04-07 |
| PRIOR PRILING DATE: 2000-04-07 |
| PRIOR PRILING DATE: 2000-04-07 |
| PRIOR PRILING DATE: 2000-04-07 |
| PRIOR FILING DATE: 2000-06-30 |
| PRIOR FILING DATE: 2000-06-30 |
| PRIOR FILING DATE: 2000-06-10 |
| WHORE NO SEQ ID NOS: 98 |
| SEQ ID NOS: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 138;
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Pred. No. 2;
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                 Sequence 1, Application US/09790988
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Best Local Similarity 47.5%;
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                 GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CRGANISM: Buchnera sp.
US-09-790-988-1
                                                                                                                                                       WATANABE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
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JS-10-204-708-28/c
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LENGTH: 11131
TYPE: DNA
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patent No. 667731

patent Normanian

patent Perpensence, Christian

patent Berent Berent State State

patent Berent Berent Normanian

patent Pill Represence: 503.1012

current Application Number: US/10/204,708

current Application Number: DE 10019058.8

prior Filling Date: 2000-04-06

prior Application Number: DE 10019173.8

prior Pilling Date: 2000-04-06

prior Pilling Date: 2000-04-06

prior Pilling Date: 2000-04-06

prior Pilling Date: 2000-04-06

prior Pilling Date: 2000-06-30

prior Pilling Date: 2000-09-01

prior Pilling Date: 2000-09-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAICAATATTTTAAAACATAATAATGATGTCTCTGAACTATGTAATTGGTTTCTACTTT 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTTTCTCTGTCACTTACCATGCATGCTTAATAAATTGATCTATCAAGCATAAAAA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 GAATAAAAGAAAGAAAAAAAAAATCAGTCAAGTAGTTGCACAACACATACTTGGAATCAAA
                                                                                                                                                                                                                                                                                                                                                304 TATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGATTAGA
                                                                                                                                                                                                                                                                           244 AAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACTAAAT
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                                                                                                                              Length 11131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 5501;
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6.9%; Score 41.4; DB 4; Length 5:
Best Local Similarity 49.8%; Pred. No. 0.82;
Matches 105; Conservative 0; Mismatches 106; Indels
                                                                                                                                                                                                          Indels
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA
US-10-204-708-28
                                                                                                                                 Query Match
6.9%; Score 41.8; DB 4;
Best Local Similarity 44.8%; Pred. No. 0.8;
Matches 160; Conservative 0; Mismatches 197;
```

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## APPLICANT: OLDEY, Alexander

APPLICANT: OLDEY, Alexander

APPLICANT: OLDEY, Alexander

APPLICANT: PRIEBENBROCK, Christian

APPLICANT: BREALIN Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

TITLE OF INVENTION: Diagnosis of Diseases Associated

TITLE OF INVENTION: DAY Assessing DNA Methylation

FILE REPERENCE: 5013.1012

CURRENT APPLICATION NUMBER: US/10/204,708

FRIOR PRILOR DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-09-01

NUMBER OF SQ ID NOS: 98

SQ ID NO 39

LENGTH: 19513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9568 AACCAAATCGCACCACTATACTCCAACCTAAATAACAAAACAAAACTCCGTCTCAAAA 9509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 AACGICACAGGAAACGAAAAAACAICAIAGAGGAIAIIIICAACAAIACCAGCCAIAIC 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             347 TACAGGACATGATTAGGAGATTTTTCACAATGATTTTTCCTACTCTTTCTGTTGTTG 406
TAGAGAGATTTTTCACAATGATTTTTCCTACTCTTTCTGTTGTGTTGAAAACCATCTTTC 419
                                                                                              AAATGAATAAAACAAAGAAAAAAAATCAGTCAAGTAGTTGCACAACACACATACTTGGAAT '479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.9%; Score 41.4; DB 4; Length 19513; Best Local Similarity 46.9%; Pred. No. 1.2; Matches 129; Conservative 0; Mismatches 146; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTIMAATAAACATAAACAATAAAATATCATA 9354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              467 ACATACTIGGAATCAAATATCAATATTTTAAAACA 501
                                                                                                                                                                                                                                                           1861 TAAAATATAAAAATAAATAAAAATAATCA 1831
                                                                                                                                                                                                        480 CAAATATCAATATTTTAAAACATAATGA 510
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 39, Application US/10204708 Patent No. 6677731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                    JS-10-204-708-39/C
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RESULT 6 US-09-468-265-4

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GARREAL INFORMATION:

APPLICANT: Cullen, Daniel

APPLICANT: Hayenga, Kirk J

APPLICANT: Hayenga, Kirk J

APPLICANT: Hayenga, Kirk J

APPLICANT: Lawlis, Virgil B

TITLE OF INVENTION: Heterologous Polypeptides Expressed in Filamentous Fungi, Process

TITLE OF INVENTION: Making Same and Vectors for Making Same

FILE REFERENCE: A-42903-5

CURRENT APPLICATION NUMBER: U8/08/468,265

CURRENT FILING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: 08/284,942

PRIOR FILING DATE: 1994-08-02

PRIOR FILING DATE: 1998-09-25

PRIOR FILING DATE: 1986-07-07

PRIOR FILING DATE: 1986-07-07

PRIOR FILING DATE: 1986-07-07

PRIOR FILING DATE: 1985-08-29

NUMBER OF SEQ ID NOS: 28

SOFTWARR: PARCENTIN VERSION 3.1

SERIOR PRIOR PRIOR PRIOR NUMBER: 06/771,374

PRIOR APPLICATION NUMBER: 06/771,374

PRIOR APPLICATION NUMBER: 06/771,374

PRIOR PR
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Patent No. 6607879

GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stidnamer
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCES: 1508
CORRESPONDENCES ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 AGTAACTACAGGACATGATTAGAGAGATTTTTCACAATGATTTTTCCTACTTTTCTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.8%; Score 41.2; DB 4; Length 1
Best Local Similarity 46.3%; Pred. No. 0.68;
Matches 136; Conservative 0; Mismatches 158; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Emericella nidulans
US-09-468-265-4
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US-09-023-655-197/c
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Sequence 29, Application US/09367895

Patent No. 648309

GENERAL INFORMATION:
PAPLICATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 078883/0112

CURRENT APPLICATION NUMBER: US/09/367,895

CURRENT FILING DATE: 1999-12-08

PRIOR PELING DATE: 1998-02-23

PRIOR PELING DATE: 1998-02-23

PRIOR PELING DATE: 1998-02-23

PRIOR PELING DATE: 1997-03-24

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 29

LENGTH 11469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368 TTTTTCACAATGATTTTTCCTACTCTTTCTGTTGTTGAAAACCATCTTTCAAATGAAT 427
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-74
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Pred. No. 1.3;
0; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                 Score 41; DB 4; Length 5152;
Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , LUCATION: (2132..2209, 3375..3494, 3812..4033, 4538..4606, 10CATION: 4753..5022, 5241..6146, 6345..6461, 6670..6732, LOCATION: 7026..7133, 7510..7611, 7784..7852, 7998..8078, 10CATION: 8321..8437, 9235..9630)
                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 100;
PRIOR FILING DATE: 2000-04-07
PRIOR PEPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4751 TAATAATCCATAAAACCAAAA 4731
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ilarity 51.4%;
Conservative
                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.2'
Matches 101; Conservative
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Best Local Similarity
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US-09-367-895-29/c
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Jeturian Description US/10204708

Jeturian Description US/10204708

Jeturian Description

APPLICANT: OLEK, Alexander

APPLICANT: PIEPENBROCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

TITLE OF INVENTION: DASSESSING DNA Methylation

FILE REFERENCE: 5013.1012

CURRENT APPLICATION NUMBER: US/10/204,708

FILE REPERSION FILING DATE: 2003-05-06

PRIOR PILING DATE: 2003-06-06

PRIOR FILING DATE: 2000-04-06

PRIOR PILING DATE: 2000-04-06

PRIOR PAPLICATION NUMBER: DE 10019058.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        457 TTTAGTAAAAAAAAAAAATATAAATGCTCTTTGCAAAGACCACCATTCATAAAATT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397 GTAAATATTTTGTATGTCAATTTCTGACATCCTTTTTACTGGGTAATTTCTGTTTTTATGC 338
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                                                    CONDUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: 1BM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION NUMBER: US/09/023,655

FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEFAX: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 197:
SEQUENCE CHARACTERISTICS:
LENGTH: 750 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
INMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.4%;
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                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LIBRARY: THP1PEB01
; CLONE: 073582
US-09-023-655-197
            CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 95; Conserv
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SEQ ID NO 29
LENGTH: 11478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11321 AAAACAATGAAAAAAAAATGAAAAAAAAAAAAAAAATTTTTCATACTCATTTGAAAAGGAAA 11262
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                       428 AAAACAAAGAAAAAAATCAGTCAAGTAGTTGCACAACACATTACTTGGAATCAAATATC 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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6.8%; Score 41; DB 3; Length 11478;
Best Local Similarity 51.4%; Pred. No. 1.3;
Matches 95; Conservative 0; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: POULSEN, PETER
TITLE OF INVENTION: INHEBITION OF GENE EXPRESSION
FILE REPERENCE: 674509-2004
CURRENT APPLICATION NUMBER: US/08/981,803
CURRENT FILING DATE: 1997-04-17
EARLIER FILING DATE: 1996-07-12
EARLIER FILING DATE: 1996-07-14
EARLIER PLING DATE: 1996-07-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTING VET: 200
SOFTWARE: PATENTING VET: 200
SOFTWARE: PATENTING VET: 200
SOFTWARE: PATENTING VET: 200
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APPLICANT: POULSEN, Peter
TITLE OF INVENTION: INHIBITION OF GENE EXPRES
TITLE REFERENCE: 674509-2003
CURRENT APPLICATION NUMBER: US/08/983,440
CURRENT FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 9514437.4
EARLIER PILING DATE: 1995-07-14
EARLIER FILING DATE: 1995-07-14
SARLIER FILING DATE: 1995-07-14
SARLIER FILING DATE: 1996-07-15
SOFTWARE: PALENTING NOS: 35
SOFTWARE: PALENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 29, Application US/08983440 Patent No. 6232122
                                                                                                                                                                                                                                                                                                                              Sequence 29, Application US/08981803
Patent No. 6147279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ; ORGANISM: Solanum tuberosum US-08-981-803-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11201 CTAČŤ 11197
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US-08-983-440-29/c
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US-08-981-803-29/c
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APPLICANT: DRUITHE, PIERRE
APPLICANT: DRUITHE, PIERRE
TITLE OF INVENTION: MALABRIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
TITLE OF TINNENTION: MALABRIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
TITLE REFERENCE: 0660-0125-0 PCT
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT APPLICATION NUMBER: US/08/94
EARLIER PILING DATE: 1996-06-12
EARLIER PILING DATE: 1996-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   428 AAAACAAAAAAAAAAAAATCAGTCAAGTAGTTGCACAACACATACTTGGAATCAAATATC
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6.8%; Score 40.8; DB 3; Length 6152;
Best Local Similarity 53.0%; Pred. No. 1.2;
Matches 87; Conservative 0; Mismatches 77; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 11478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.8%; Score 41; DB 3;
51.4%; Pred. No. 1.3;
                                                                                                                   or C or T/U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          or T/D
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: variation
LOCATION: (1)..(11478)
CTHER INFORMATION: M stands for A or
US-08-983-440-29
                                                                                                                                                                                                                                                                                                                or
                                                                                                                                                                                                                                                          NAME/KEY: variation
LOCATION: (1)...(11478)
LOCATION: (1)...(11478)
FRATURE: Variation: K stands for G or
NAME/KEY: variation
LOCATION: (1)...(11478)
OTHER INFORMATION: W stands for A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-08-973-462-1
Sequence 1, Application US/08973462B
; Patent No. 6191270
; GENERAL INFORMATION:
                                                                                                                          FEATURE:
NAME/KEY: variation
NAME/KEY: variation
OCHER INFORMATION: R stands for G PRATURE:
                                                                     NAME/KEY: variation
LOCATION: (1)..(11478)
OTHER INFORMATION: B stands for G
TYPE: DNA
ORGANISM: Solanum tuberosum
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Best Local Similarity 51.4
Matches 95; Conservative
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AAATGAATAAAACAAAGAAAAAAAATCAGTCAAGTAGTTGCACAACACATACTTGGAAT 479
                                         425 AATAAAACAAAGAAAAAAAATCAGTCAAGTAGTTGCACAACACATTGGAATCAAAT 484
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                                                                                     CAAATATCAATATTTTAAAACATAATAATGATAGTCTCTGAACTATGTAATTGGTTTCTA
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APPLICANT: WALLACH, MICHARL, PUGATSCH, THRA, MENCHER, DAVID
TITLE OF INVENTION: METHOD OF REDUCING THE OUTPUT OF EIMERIA
COCYSTS FROM A NUMBER: 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/108,763
FILING DATE: 17-AUG-1993
PRICH PAPLICATION DATA:
APPLICATION NUMBER: 310,603
FILING DATE: 16-JAN-1991
APPLICATION NUMBER: 310,603
FILING DATE: 11-FEB-1989
PILING DATE: 11-FEB-1989
PILING DATE: 11-FEB-1989
PILING DATE: 11-FEB-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 465;
                                                                                                                                                                       540 CTTTCTTTTCTCTGTCACTTACCATGCTTAATAAATTGAT 583
                                                                                                                                                                                                                 429 TATTATCTTTTAGTCTGATATAACAAGAGTTGGAAAAAAA 472
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Pred. No. 0.71;
0; Mismatches 86;
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FILING DATE: 17-AUG-193
APPLICATION DATA:
APPLICATION NUMBER: 642,219
FILING DATE: 16-JAN-1991
APPLICATION NUMBER: 310,603
FILING DATE: 14-FEB-1989
APPLICATION NUMBER: 155,245
FILING DATE: 12-FEB-1988
APPLICATION NUMBER: 996,611
FILING DATE: 14-AUG-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 896,611
FILING DATE: 14-AUG-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 51.7%;
Matches 92; Conservative 0
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5496550-7
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                                                                                                                                                                                                                                                                                                                       APPLICANT: DRUILER.
APPLICANT: DRUILER.
APPLICANT: DRUBERSIES, PIERRE
APPLICANT: DRUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT FILING DATE: 1998-02-06
BARLIER FILING DATE: 1996-06-13
EARLIER FILING DATE: 1996-06-13
SARLIER APPLICATION NUMBER: FR 95/07007
EARLIER APPLICATION NUMBER: FR 95/07007
SARLIER APPLICATION NUMBER: 1995-06-13
SOFTWARE: PATENTIN VOY: 2.0
SEQ ID NOS: 29
SOFTWARE: PATENTIN VOY: 2.0
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                                                                                                                                      86; Indels
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                                                                                       Score 40.4; DB Pred. No. 0.71; 0; Mismatches
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6.7%; Score 40.2; DE
Best Local Similarity 56.4%; Pred. No. 1.6;
Matches 75; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08973462B Patent No. 6191270 GENERAL INFORMATION:
                                                                                       6.7%;
ilarity 51.7%;
Conservative (
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; ORGANISM: P. falciparum
US-08-973-462-1
                                                                                                           1 Similarity
92; Conserv
         LENGTH: 466
5496550-7
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Best Local S:
Matches 92
SEQ ID NO:7:
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Job time
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August 15, 2004, 21:45:13; Search time 386 Seconds (without alignments) 7677.697 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_DEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 4, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 15, Appl	Sequence 200, App	Sequence 3, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli
ДI	US-10-079-754A-4	US-10-079-754A-1	US-10-079-754A-2	US-10-079-754A-6	US-10-079-754A-15	US-10-079-623-200	US-10-079-754A-3	US-10-079-754A-5	US-09-992-600A-5	US-09-924-340-5	US-09-992-095B-5	US-09-999-570-5	US-10-000-489-5	US-10-000-986-5
	14	14	14	14	14	14	14	14	10	10	10	10	15	15
% Query Match Length DB	604	505	585	525	267	267	869	96	438	438	438	438	438	438
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Score	604	465.4	448.2	423.4	238.4	238.4	115	87	70.4	70.4	70.4	70.4	70.4	70.4
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US-10-154-678-5	US-10-001-142-5	US-10-210-172-167	US-10-104-047-1193	US-10-027-632-263847	-10-027-	US-10-027-632-263849	-10-027-	-10-027-632-	-10-027-6	-10-115-635-30	US-10-311-455-1358	US-10-312-841-2	10-311-455-9	US-10-311-455-271	US-10-221-714A-381	-10-312-841-	0-311-455-1	10-31	.0-311-45	ū	-10-311-45	-10-240-589C-12	10-424-599-14	5-75	-10-221-714A-	-10-172-086-1	US-10-311-507-35	5-73	-10-240-45	US-10-240-589C-74
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ALIGNMENTS

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   GENERAL INFORMATION:

GENERAL INFORMATION:

Publication No. US20020164625A1

GENERAL INFORMATION:

APPLICANT: Glenn, Matthew

APPLICANT: Glenn, Matthew

APPLICANT: Grigor, Murray R.

APPLICANT: Molenar, Adrian J.

APPLICANT: Davis, Stephen R.

TITLE OF INVENTION: Compositions Isolated from Bovine

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TITLE OF INVENTION: Compositions Isolated from Bovine

TITLE OF INVENTION: Compositions Isolated from Bovine

TITLE OF INVENTION: Compositions Isolated from Bovine

TITLE OF INVENTION: UNDER: US 09/699,146

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 1999-10-29

PRIOR APPLICATION NUMBER: US 60,150,330

PRIOR APPLICATION NUMBER: US 60,150,330
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100.0%; Score 604; DB 14;
Best Local Similarity 100.0%; Pred. No. 4.9e-128;
Matches 604; Conservative 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Bovine
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Query Match

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133 CAGGACTCCACCAAATATGAAGATCTTTATCTTTATCTTCATTATGGCTCTCATCCTAGC
Best Local Similarity 99.8%; Pred. No. 2.1e-96; Matches 466; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 99.3
Matches 450; Conservative
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ORGANISM: Bovine
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                                                                     GGATTTCAAGGTATTTAAACACAGCAGTTTTCTAGCAAAGAACATCTCCTGAAGCATCAG
                                                                                                                       AATTICATCTTTCATGACTGGACTCCACAAATATGAAGATCTTTATCTTTGTCTTCATT
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APPLICANT: Glenn, Matthew
APPLICANT: Grigor, Murray R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Compositions 10010/68
CURRENT APPLICATION NUMBER: US 09/699,146
FRICAR APPLICATION NUMBER: US 09/699,146
FRICAR APPLICATION NUMBER: US 09/699,146
FRICAR FILING DATE: 1999-10-29
FRICAR FILING DATE: 1999-10-29
FRICAR FILING DATE: 2000-08-22
FRICAR APPLICATION NUMBER: US 60,162,701
FRICAR FILING DATE: 1099-10-29
FRICAR FILING DATE: 1099-10-29
FRICAR FILING DATE: 1099-10-29
FRICAR FILING DATE: 1099-10-29
FRICAR FILING DATE: 1099-10-29
FRICAR FILING DATE: 1099-10-29
FRICAR FILING DATE: 1099-10-29
FRICAR APPLICATION NUMBER: US 60,150,330
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 505
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Sequence 2, Application US/10079754A

Publication No. US2020164625A1

GENERAL INFORMATION:

APPLICANT: Glenn, Matthew

APPLICANT: Glenn, Matthew

APPLICANT: Glenn, Matthew

APPLICANT: Molenari, Adrian J.

APPLICANT: Davis, Stephen R.

ITILE OF INVENTION: Compositions Isolated from Bovine

ITILE OF INVENTION: Compositions Isolated from Bovine

ITILE OF INVENTION: Mammary Gland and Methods for Their Use

ITILE OF INVENTION: UNBER: US/10/079,754A

CURRENT FILING DATE: 2002-02-19

PRIOR APPLICATION NUMBER: US 09/699,146

PRIOR APPLICATION NUMBER: US 09/699,146

PRIOR APPLICATION NUMBER: US 09/644,190

PRIOR FILING DATE: 1999-10-29

PRIOR PILING DATE: 1999-10-29

PRIOR PILING DATE: 1999-08-23

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0

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APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Grigor, Murray R.
APPLICANT: Mammary Gridor Grow Bovine
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Mammary Gland and Methods for Their Use
FILE REFERENCE: 11000-1068
CURRENT APPLICATION NUMBER: US/10/079,754A
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 09/699,146
PRIOR APPLICATION NUMBER: US 09/644,190
PRIOR APPLICATION NUMBER: US 09/644,190
PRIOR APPLICATION NUMBER: US 09/644,190
PRIOR FILING DATE: 1999-08-22
PRIOR APPLICATION NUMBER: US 60,150,330
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 99.6
Matches 239; Conservative
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US-10-079-754A-15
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                                                                    AGGATATTTTCAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTA 317
                                                                                                                                   253 AGGATATTITCAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTGCGTA 312
                                                                                                                                                                                        TCCATITCCTIAAAATGCTGCTTAGTAACTACAGGACATGATTAGAGAGATTTTTCACAA 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                       498 AACATAATAATGATAGTCTCTGAACTATGTAATTGGTTTCTACTTTTCTTTTCTGTCAC
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                                                                                                                                                                                                                                                                                                                                                     438 AAAAAAATCAGTCAAGTAGTTGCACAACACATACTTGGAATCAAATATGTTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovine
for Their Use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/10079754A

Publication No. US20020164625A1

GENERAL INFORMATION

APPLICANT: Glenn, Matthew

APPLICANT: Glenn, Matthew

APPLICANT: Glenn, Matthew

APPLICANT: Molenear, Aditan J.

APPLICANT: Davis, Stephen R.

TITLE OF INVENTION: Compositions Isolated from Bov.

TITLE OF INVENTION: Mammary Gland and Methods for

TITLE OF INVENTION: Mammary Gland and Methods for

TITLE OF INVENTION: MUMBER: US/10/079,754A

CURRENT APPLICATION NUMBER: US 09/699,146

PRIOR APPLICATION NUMBER: US 09/699,146

PRIOR FILING DATE: 2000-10-27

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 2000-08-22

PRIOR APPLICATION NUMBER: US 60,162,701

PRIOR FILING DATE: 2000-08-22

PRIOR APPLICATION NUMBER: US 60,150,330

PRIOR PILING DATE: 1999-10-29

PRIOR APPLICATION NUMBER: US 60,150,330

PRIOR FILING DATE: 1999-10-23

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FRSESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         558 TTACCATGCATGCTTAATAAATTGATCTATCAA 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   553 TTACCATGCTTAATAAATTGATCTATCAA 585
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LENGIH: 525
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87

257 147 317 207

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TYPE: DNA
CRGANISM: Bovine
US-10-079-754A-3
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US-10-079-754A-5
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US-09-992-600A-5
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SEQ ID NO 3
LENGTH: 869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 AGGATATITICAACAATACCAGCCATATCAACGATATCCACTAAATTATCCTCCTGCGTA
                                                                                                                                                                                                    Sequence 200. Application US/10079623
| Publication No. US20020169302A1
| GENERAL INFORMATION:
| APPLICANT: Harvakkala, Ilkka J.
| APPLICANT: Glenn, Matthew
| APPLICANT: Glien, Matthew
| APPLICANT: Glien, Matthew
| APPLICANT: Glien, Matthew
| TITLE OF INVENTION: Compositions isolated from bovine
| TITLE OF INVENTION: mammary gland and methods for their use.
| TITLE OF INVENTION: mammary gland and methods for their use.
| TITLE OF INVENTION: WORDS: 11000.1004463
| CURRENT FILICATION NUMBER: US/10/79,623
| CURRENT FILICATION NUMBER: US/10/202-02-19
| NUMBER OF SEQ ID NOS: 370
| SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20020164625A1

Publication No. US20020164625A1

APPLICANT: Grigor, Murray R.

APPLICANT: Grigor, Murray R.

APPLICANT: Molenar, Adrian J.

APPLICANT: Molenar, Adrian J.

APPLICANT: Molenar, Adrian J.

APPLICANT: Molenar, Adrian J.

APPLICANT: Molenar, Adrian J.

APPLICANT: Molenar, Adrian J.

APPLICANT: Molenar, Adrian J.

APPLICANT: Molenar, Adrian J.

APPLICANT: Molenar, Adrian J.

APPLICANT: Molenar, Adrian J.

PRIME REFERENCE: 11000.1068

CURRENT APPLICATION NUMBER: US/10/079,754A

CURRENT FILING DATE: 2002-02-19

PRIOR FILING DATE: 2000-01-027

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 1999-00-33

PRIOR FILING DATE: 1999-00-23

PRIOR FILING DATE: 1999-08-23

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Bovine
                                                                                                                                                             RESULT 6
US-10-079-623-200
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LENGTH: 267
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GENERAL INFURMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Grigor, Muray R.
APPLICANT: Manar, Adrian J.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
TITLE OF INVENTION: Manmary Gland and Methods for Their Use
FILE REFERENCE: 11000.1068
CURRENT APPLICATION NUMBER: US/10/079,754A
CURRENT APPLICATION NUMBER: US 60,162,701
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 5
LENTING DATE: 96
   Length 869;
Query Match
19.0%; Score 115; DB .14; Length 86
Best Local Similarity 92.4%; Pred. No. 3.3e-16;
Matches 121; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 14.4%; Score 87; DB 14; Length 96; Similarity 94.7%; Pred. No. 2.8e-10; 90; Conservative 0; Mismatches 5; Indels
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                                                                                                                         138 CTGGACTCCACCAAATATGAAGATCTTTATC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 5, Application US/10079754A; Publication No. US20020164625A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                    258 AGGATATTTTC 268
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Matches 90; Conserv
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ORGANISM: Bovine
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PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SEQ ID NO 5
LENGTH: 438
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Best Local Similarity 69.9%;
Matches 95; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: 84..317
                                                                                                                                                                                                 NAME/KEY: 5'UTR
LOCATION: 1..83
NAME/KEY: CDS
LOCATION: 84..31'
NAME/KEY: 3'UTR
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LOCATION: 1..83
                                                                                                                                                                                                                                                                                                              LOCATION: 318...
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US-09-992-095B-5
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LENGTH: 42
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APPLICANT: Bejain, Stephane
APPLICANT: Banaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REPERENCE: 91.US2.RSG
CURRENT APPLICATION NUMBER: US/09/924,340
CURRENT FILMG DATE: 2001-08-06
PRIOR PELING DATE: 2001-08-06
PRIOR PELING DATE: 2001-07-13
PRIOR PELING DATE: 2001-07-13
PRIOR PELING DATE: 2001-06-29
PRIOR PELING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR PLING DATE: 2001-06-19
PRIOR PILING DATE: 2001-06-15
           TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 70.4; DB 10; Length 4 Pred. No. 3.6e-06; 0; Mismatches 41; Indels
                       TILLE REPERENCE: 91.034.DIV
CURRENT APPLICATION NUMBER: US/09/992,600A
CURRENT FILING DATE: 2001-11-13
CURRENT FILING DATE: 2001-11-13
PRIOR PRILOR APPLICATION NUMBER: US 09/924,340
PRIOR PRILOR APPLICATION NUMBER: US 06/305,456
PRIOR FILING DATE: 2001-08-06
PRIOR PRILOR DATE: 2001-07-13
PRIOR PRILOR DATE: 2001-07-13
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 114
SEQ ID NO 5
LENGTH: 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 ACGGAAAAAACATCAT 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 69.9%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: polyA_signal
LOCATION: 397..402
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: 423..438
US-09-992-600A-5
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LOCATION: 318..438
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LOCATION: 84..317
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LOCATION: 1..83
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APPLICANT: Tanaka, Hiroaki
TITE.OF INVENTULON: HIMAN CDNAS AND PROTEINS AND USES THEREOF
FILTE OF INVENTULON: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILTE OF INVENTULON: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILT STEPENT APPLICATION NUMBER: US/09/992,095B
CURRENT APPLICATION NUMBER: US/09/924,340
PRIOR APPLICATION NUMBER: US/09/924,340
PRIOR PILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US/0305,456
PRIOR APPLICATION NUMBER: US/0305,456
PRIOR APPLICATION NUMBER: US/0305,456
PRIOR APPLICATION NUMBER: US/0305,456
PRIOR PILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US/05/293,574
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    Length 438;
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Score 70.4; DB 10; Length
Pred. No. 3.6e-06;
0; Mismatches 41; Indels
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US-10-000-489-5; Application US/10000489; Bedrance 5; Application US/10000489; Publication No. US20030092011A1; GENERAL INFORMATION:
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| NAME/KEY: CDS
| LOCATION: 64..31
| LOCATION: 318..438
| NAME/KEY: polyA signal
| LOCATION: 397..402
| NAME/KEY: polyA signal
| LOCATION: 423..438
| US-10-000-489-5
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LOCATION: 1..83
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APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TILE OF INVENTION: HUMAN CONAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: G-091USOBDIV
CURRENT FILING DATE: 2001-06-14
FRICH APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
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PRIOR PLICATION NUMBER: US 60/302,277
PRIOR PLICATION NUMBER: US 60/302,277
PRIOR PLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-25
PRIOR PLING DATE: 2001-06-25
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PRIOR FILING DATE: 2001-06-25
PRIOR PLING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-06-15
PRIOR PLENGTH: 438
TYDE: DATE: DATE: 2001-06-15
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Pred. No. 3.6e-06;
0; Mismatches 41; Indels 0
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Best Local Similarity 69.9%;
Matches 95; Conservative
                                                                                   NAME/KEY: polyA signal LOCATION: 397..402
FEATURE:
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ORGANISM: Homo sapiens
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LOCATION: 397..402
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// LOCATION: 423..438
US-09-992-095B-5
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; LOCATION: 423..438
US-09-999-570-5
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LOCATION: 318..438
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LOCATION: 84..317
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NAME/KEY: 5'UTR
LOCATION: 1..83
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APPLICANT: Tanaka, Hiroaki
TITLEO PO INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REPERRICE: 91.086.DIV
CURRENT APPLICATION HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REPERRICE: 91.086.DIV
CURRENT APPLICATION NUMBER: US/10/000,489
CURRENT APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR PILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR PILING DATE: 2001-08-06
PRIOR PLING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR PILING DATE: 2001-06-15
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No. 3.6e-06; Conservative 0; Mismatches 41; Indels 0
Query Match
Best Local Similarity 69.9%; Pred. No. 3.6e-06;
Matches 95; Conservative 0; Mismatches 41; Indels 0
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APPLICANT: Benjamin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.U59.DIV
CURRENT FILING DATE: 2001-11-14
FRIOR FILING DATE: 2001-11-14
FRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
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PRIOR FILING DATE: 2001-06-25
SOFTWARE: JABURATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-06-25
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PRIOR FILING DATE: 2001-06-25
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Sequence 5, Application US/10154678
Publication No. US20030162186A1
GENERAL INFORMATION:
APPLICANT: Benjamin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUVAN CDNAS AND PROTEINS AND USES THEREOF
FILE REPERENCE: 182.US1.REG
CURRENT APPLICATION NUMBER: US/10/154,678
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Pred. No. 3.6e-06;
0; Mismatches 41;
                                                                                                                            RESULT 14
US-10-000-986-5
Sequence 5, Application US/10000986
Publication No. US20030096247A1
GENERAL INFORMATION:
170 TAGAAGAAATTCCAT 185
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Best Local Similarity 69.9%;
Matches 95; Conservative
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NAME/KEY: polyA signal
LOCATION: 397..402
NAME/KEY: polyA site
LOCATION: 423..438
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ORGANISM: Homo sapiens
FEATURE:
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LOCATION: 1..83
NAME/KEY: CDS
LOCATION: 84..317
NAME/KEY: 3'UTR
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CURRENT FILING DATE: 2002-10-15
PRICR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-15
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NAME/KEY: polyA_signal
LOCATION: 397..402
FEATURE:
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; LOCATION: 423..438
US-10-154-678-5
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LOCATION: 84..317
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CB984475 AGENCOURT CB98521 AGENCOURT CB987745 AGENCOURT BX485825 DKFZp686L BX485714 DKFZp686E CB987175 AGENCOURT

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Perfect score:

Sequence:

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Run

Scoring table:

Searched:

Database

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Homo sapiens (nument, substance) (contacts) Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 533)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabb-:ramail.nih.gov

Tissue Procurement: Dr. Midhael Brownstein and Dr. Miklos Palkovits cDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Parayed by: The I.M.A.G.E. Consortium (LLML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: NDCM443 row: b column: 08

High quality sequence stop: 553.
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                                                              BX485714
CB987175
AA376700
AA382524
AA376704
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KEYWORDS
SOURCE
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DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
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CB985810
 CB985810 AGENCOURT
CB957544 AGENCOURT
CB986888 AGENCOURT
CB958289 AGENCOURT
                                                                                                   August 15, 2004, 07:37:23 ; Search time 2272 Seconds (without alignments) 7938.713 Million cell updates/sec
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604
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             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                        nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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13.0
13.0
13.0
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82.2 78.6 78.6 78.6

Score

Result No.

'organism="Homo sapiens"

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/do_xret="InAGG:3029983"
/lab_host="IMAGG:3029983"
/lab_host="DH10B (T1 phage-resistant)"
/clone=lib="NIH MGC 184"
/clone lib="NIH MGC 184"
/note="Organ: Pooled-Glandlar; Vector: pDNR-LIB; Site_1:
Sfil (ggccattatggcc); Site_2: Sfil (ggccgctcggcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyoid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5' CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCGGGGCGACATG-GT(30) BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contendined inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
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These Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be thrup://image.llnigov

http://image.llnigov

Louint: Tow: I column: 17
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1 (bases 1 to 546)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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B
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IMAGE:30352504 5', mRNA sequence.
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                                                  'organism="Homo sapiens"
'mol_type="mRNA"
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Location/Qualifiers
                                                                                                                  _xref="taxon:9606"
ocation/Qualifiers
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/Lib host="Implies" In plage resistant)"
/lab host="DHIOR" (TI phage resistant)"
/clone lib=NIH MGC 184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_I:
SfiI (sgccattatgggcc); Site_2: SfiI (ggccgctcggcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyoid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5' -CACGCCATTATGGCC-3' and 3' adaptor sequence:
5' -ATTATAGAGGCGGGGGGGCGCATG-(130) BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0. 60-3: kb). 15/15 colonies contrained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
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Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

CDN Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDCM441 row: k column: 23

High quality sequence stop: 551.
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1 (bases 1 to 555)
NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AGENCOURT 13650592 NIH MGC_184 Homo sapiens cDNA clone
IMAGE:30329446 5', mRNA sequence.
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hea 94; Indels
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30352504"
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Nutional Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONIECH Laboratories, Inc.
cDNA Library Preparation: CLONIECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIAL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIAL at:
http://image.llnl.gov
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Email: Gapba-remail.inh.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LIANL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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1. (Dases 1 to 793)

NIH-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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/lab host="MINDB (TI phage-resistant)"
/lab host="MINDB (TI phage-resistant)"
/lone="Grgan: Pooled-Glandular; Vector: pDNR-LIB; Site_I:
Sfil (sgccactateggc); Site_2: Sfil (ggccactateggc);
Library is oligo-dT primed and directionally cloned. contactly color a glandular pool of tissues from thyoid, parathyroid, adrenal, cortex and pineal gland. S' and 3' adaptors were used in cloning as follows: S' adaptor sequence: S'-ATCTRAGGCCATTATGGCC-3' and 3' adaptor sequence: S'-ATCTRAGGCCAGGCGAGGCGCGACAG-dT(3)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb): 15.15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clonech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

CDNA Library Preparation: CLONIECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Best Local Similarity 60.2%; Pred. No. 0.0014;
Matches 151; Conservative 0; Mismatches 94; Indels 6;
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AGENCOURT_13652179 NIH_MGC_184 Homo sapiens cDNA clone
IMAGES30327553 5', mRNA sequence.
found through the I.M.A.G.E. Consortium/LLNL at:
                      http://image.llnl.gov
Plate: NDCM135 row: h column: 14
High quality sequence scop: 486.
Location/Qualifiers
                                                                                                                                                     'organism="Homo sapiens"
                                                                                                                                                                                     mol_type="mRNA"
db_xref="taxon:9606"
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AGENCOURT 13621497 NIH MGC 184 Homo sapiens cDNA clone
MAGE:30327757 5', mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 929)
                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: NDCMIS row: m column: 02
High quality sequence stop: 177.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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DNA Sequencing by: Agencourt Bioscience Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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DKPZp686L09248 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DAREGBEL09248 5', mRNA sequence.
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 583)
Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W.,
Mamil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
EST (Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W.,
et al.)
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cDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: Plate: NDCM137 row: e column: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                               13.0%; Score 78.6; DB 14;
Llarity 60.2%; Pred. No. 0.0013;
Conservative 0; Mismatches 94;
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Best Local Similarity
Matches 151; Conserv
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BX485825
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622 bp mRNA linear EST 04-SEP-2003
DKFZEP666E20248 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKF2F686E20248 5', mRNA sequence.
                                                                                                                          sequenced by MediGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. No s1 sequence available.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97
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(Dases 1 to 622)

Ottenwaelder, D., Obermaier, B., Deutschenbaur, S., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S. EST (Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hlcc3)"
Site_1: SfiIA, Site_2: SfiIB,
                                                                                                                                                                                                                                                         This clone (DKPZp686L09248) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
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Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Can
Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de,
sequenced by MediGenomix (Martinsried/Germany) within the cD
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Similarity 56.2%; Pred. No. 0.0023;
19; Conservative 0; Mismatches 139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult"
/lab_host="DH10B"
/clone lib="686 (synonym: h'note="Vector: pTriplEx2; s_cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="DKFZp686L09248"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
                                   Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insart
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center. (DKP2); Email s.wiemann@dkfz-heidelberg.de,
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No s1 sequence
available.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 773)
                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="686 (synonym: hlcc3)"
//note="vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB;
                                                                                                                                                                                            This clone (DKFZp686E20248) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AGENCOURT 13650773 NIH MGC 184 Homo sapiens cDNA clone IMAGE:30329891 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                         'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                            'mol_type="mRNA"
'db_xref="taxon:9606"
'clone="DKF2p686E20248"
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/lab_host="DH108"
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1 (Dases 1 to 312)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.G., Lee, N.H., Kirkness, E.F., Weinstrock, K.G., Goosayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
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cDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Apencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
http://image.lln.gov
Plate: NDCM142 row: n column: 12
High quality sequence stop: 181.
Location/Qualifiers
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Best Local Similarity
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Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, F.S.T., Kelley, J.M., Kelley, J.M., Kelley, J.M., Kelley, J.M., Moreno-Palanques, R.F., McDould, L.A., Nguyen, D.T., Merrick, J.M., Moreno-Palanques, R.F., McDould, L.A., Nguyen, D.T., Pelligrino, S.M., Shalley, C.A., Ryder, S.B., Scott, J.L., Saudek, D.M., Shritey, R., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Y., Bednarik, D.P., Cao, L.F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.M., Hu, J.S., Greene, J.M., Greene, J.M., Grastings, G.A., Kozak, D.L., Kunsch, C., Hunglun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Li, H., Meissner, P.S., Olsen, H., Praser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
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Sor clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
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12.7%; Score 77; DB 9; Length 312;
Best Local Similarity 59.8%; Pred. No. 0.004;
Matches 150; Conservative 0; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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Location/Qualifiers
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Bioinformatics
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AA382524
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EST 21-APR-1997

AA382524 327 21-APR-199 SET95743 Testis I Homo sapiens CDNA 5' end similar to histatin 1, mRNA sequence. AA382524

DEFINITION

ACCESSION

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The dames, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bult, C.J., Lee, N.H., Kirkness, E.F., Wenstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Fitzgeraid, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Glodek, A., Gnehm, C.L., Lui, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, J.F., Lui, Y.,

Bednarik, D.P., Feng, D.-F., Ferrie, A., Gruber, J., Hudson, P., Kim, A.K.,

Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,

Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Rubben, S.M.,

Billion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,

Fraser, C.M. and Venerer, J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 cricocricardaririccardariracccricarircacardaaaagagacarcargagra 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 ACGGAAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 TAGAAGAAATTCCAT----GAAAAGCATCATTCACATCGAGAATTTCCATTTATGG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: arkerlav@tigr.org

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

Information related to this EST, please check the TIGR Human Gene

Index (http://www.tigr.org/tdb/hgi/hgi.html)

Seq primer: M13 Reverse.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
                              Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 GACTCTCCTCTTGAGTAAAGGACTCAGCCAACTATGAAGTTTTTTTGTCTTTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 TATGGCTCTCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
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llarity 59.8%; Pred. No. 0.0039;
Conservative 0; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Other ESTs: THC102726
Contact: Kerlavage, AR
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bioinformatics
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Best Local Similarity
Matches 150; Conserv
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Manuality Burners, Figures, Continued of Manuality Burners, E. Manuality Burners, E. Manuality Burners, E. Manuality Burners, E. Manuality, C. Manuality, C. Manuality, C. Sutton, G. Blake, J. M. Brandon, R.C., Manualic, Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Manualic, C., Sutton, G., Hanna, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hachlom, E., Hinkle, P. S.J., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Benarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Liw, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Rozak, D.L., Kunsch, C., Hungjun, J., Li, H., Maissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, R., Rosen, C.A., Haseltine, W.A., Fields, C., Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA376689 348 bp mRNA linear EST 21-APR-1997 EST69145 Salivary gland Homo sapiens CDNA 5' end similar to histatin 1, mRNA sequence.
                                             76 criedcicicaleatriceateatracecricatreacateaaaadacateateata 135
                                                                                                         240 ACGGAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT 299
                                                                                                                                                               136 TAGAAGAAATTCCAT----GAAAAGCATCATTCACATCGAGAATTTCCATTTATGG 189
                                                                                                                                                                                                                        300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT 359
                                                                                                                                                                                                                                                                           Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAAACGTCACAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Other ESTs: EST89144 THC102726
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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AA376689.1 GI:2029007
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                                                                                                                                                                                                                                                                                                                                             360 TAGAGAGATTT 370
                                                                                                                                                                                                                                                                                                                                                                                                   250 raragaggrir 260
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COMMENT
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AUTHORS
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AA376689
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Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr.,

Kelley, J.M., Kalley, J.C., Liu, L.I., Marmaros, S.M., Merrick, J.M.,

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Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,

Raymond, L., Wei, Y.F., Wing, J., Li, H., Meissner, P.S., Olsen, H.,

Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of CDNA sequence
                                                                                                                                                                                                   330 bp mRNA linear EST 21-APR-1997
EST89161 Salivary gland Homo sapiens CDNA 5' end similar to
haratin 1, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75
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Site_1: EcoRI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 GACTCTCCTCTTGAGTAAAAGGACTCAGCCAACTATGAAGTTTTTTTGTCTTTAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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/db_xref="taxon:9606"
/dev_stage="adult"
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1larity 59.8%; Pred. No. 0.0038;
Conservative 0; Mismatches 95
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Contact: Kerlavage, AR
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                                                                                                   258 TATAGAGGTTT 268
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                                                360 TAGAGAGATTT
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I (bases 1 to 390)

Sebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.
Human UnigeneSet - RZPD3

L Unpublished (2003)

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Petel 580, D-69120 Heidelberg, Germany

RZPD IMAGPSSN191131.

RZPDILB; I.M.A.G.E. cDNA Clone Collection;

Human UnigeneSet - RZPD3 (RZPDILB No.972)

http://www.rzpd.de/CloneCards/Cgi-
bin/showlib.pl.cgi/response?libNo-972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Fax: +49 30 32639 101

www.rzpd.d.d.
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                                                                                                                                                                                                                                                                       180 TATGGCTCTCATCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA 239
                                                                                                                                                                                                                                                                                                                       CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAAGAGACATCATGGGTA 131
                                                                                                                                                                                                                                                                                                                                                                         240 ACGGAAAAAACATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT 299
                                                                                                                                                                                                                                                                                                                                                                                                                        132 TAGAAGAAATTCCAT----GAAAAGCATCATTCACATCGAGAATTTCCATTTTATGG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 AAATTATCCTCCTGCGTATCCATTTCCTTAAAATGCTGCTTAGTAACTACAGGACATGAT 359
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/note="Organ: muscle" (skeletal); Vector: pDNR-LIB
(Clontech); Site 1: Sfil (ggcggctcggctcggc); Site 2: Sfil
(Ggccattatggcc); Site 2: Sfil
(Ggccattatggcc); Site 5: Adaptors were used in cloning
as follows: S. adaptor sequence: S'-CACGGCATTATGGCC-3.
                                                                                                                                                                                                                     12 GACTCTCCTCTTGAGTAAAAGGACTCAGCCAACTATGAAGTTTTTTGTCTTTTGGT 71
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9
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                                                                         Length 348;
                                                                    Score 77; DB 9; Length 348
Pred. No. 0.0038;
0; Mismatches 95; Indels
Site_1: EcoRI; Site_2: XhoI"
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                                                                    12.7%;
ilarity 59.8%;
Conservative
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Homo sapiens
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                                                               Query Match
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Matches 150; Conserv
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and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGCACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."
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Pred. No. 0.0036;
0; Mismatches 95; Indels
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Best Local Similarity 59.8%;
Matches 150; Conservative
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